

# Personalized Oncology Through Integrative High-Throughput Sequencing: A Pilot Study

## Supplementary Appendix

### I. Supplementary Results..... Page 2

- Patient 2, Prostate cancer xenograft, Results
- Patient 4, Metastatic melanoma, Results

### II. Supplementary Methods ..... Page 3

#### **Study Design**

- Flexible default informed consent

#### **Sample Processing**

- Sample and Sequencing Library Preparation
- Sequencing quality control
- Sanger sequencing to validate novel somatic point mutations

#### **Bioinformatics Methods**

- Bowtie/In-house somatic variant calling pipeline
- GATK variant calling pipeline
- Annotation of point mutation calls
- Structural rearrangements and copy number alteration detection from whole genome sequencing
- Copy number alteration detection from exome sequencing
- Tumor content estimation from exome sequencing data
- Gene fusion discovery from RNA-Seq
- Outlier analysis from RNA-Seq
- Integration of multiple sequencing modalities

### III. Supplementary Discussion..... Page 9

- Sequencing strategies
- Bioinformatics strategies
- Accuracy of structural variation detection
- Coverage of clinically significant mutations
- Costs associated with integrative high-throughput sequencing
- Limitations of integrative sequencing

### IV. Supplementary References..... Page 11

### V. Supplementary Figures and Legends..... Page 14

- Figure S1: Integrative sequencing of a patient's prostate cancer xenograft.
- Figure S2: Additional aberrations reported in Patient 1 (Prostate cancer xenograft).
- Figure S3: Aberrations reported in Patient 2 (Prostate cancer xenograft)
- Figure S4: Additional aberrations reported in Patient 3 (Colorectal cancer)
- Figure S5: Aberrations reported in Patient 4 (Melanoma)
- Figure S6: Bioinformatics workflow diagram
- Figure S7: Tumor content estimation by pathology and in silico methods

- Figure S8: Integrative sequencing coverage of COSMIC mutations
- Figure S9: Projections for Cost of Integrative Sequencing

**VI. Supplementary Tables..... Page 24**

- Table S1: Breakdown of costs associated with integrative sequencing
- Table S2: Sequencing tumor board expertise
- Table S3: Informative gene list
- Table S4: Patient information
- Table S5: Alignment statistics
- Table S6: Somatic variants: Patient 1
- Table S7: Somatic variants: Patient 2
- Table S8: Somatic variants: Patient 3
- Table S9: Somatic variants: Patient 4
- Table S10: Germline variants: Patient 3
- Table S11: Germline variants: Patient 4
- Table S12: Copy number alterations by patient
- Table S13: Structural variants by patient
- Table S14: Gene fusions: Patient 1
- Table S15: Gene fusions: Patient 2
- Table S16: Gene fusions: Patient 3
- Table S17: Gene fusions: Patient 4

**I. Supplementary Results**

**Patient 2, Prostate cancer xenograft, Results**

Patient 2 is a 60-year-old man with metastatic prostate cancer not yet treated with hormonal therapies. The patient presented with metastatic bone disease and the xenograft was created from a bone marrow biopsy. Tumor content was estimated to be greater than 90% (**Figure S7**). Integrative sequencing identified 127 point mutations, 151 CNAs, 169 rearrangements, and 13 gene fusions. Copy number analysis revealed a one-copy loss of TP53 and a homozygous deletion of PTEN based on tumor exome and whole genome data (**Figure S3**). RNA-seq identified the presence of the TMPRSS2-ERG gene fusion, which also was detected via whole genome sequencing based on an interstitial deletion (**Figure S3**). RNA-seq and whole genome sequencing revealed a reciprocal translocation involving the 5' UTR of TP53 (not shown). RNA-seq outlier analysis revealed striking expression of Polo-like kinase 1 (PLK1).

The mock STB deliberated on the clinical significance of nominated aberrations for both prostate cancer cases. Recent preclinical studies support a rationale for PARP inhibitors in ERG-rearranged prostate cancer(*1*). Further, amplification of AR implies intact androgen signaling in the tumor, and loss of PTEN supports a possible role of the PI3K pathway(*2*). Recent data suggests that combined blockade of these two pathways may provide additional benefit over single agent therapy(*3*). The STB determined that the gene fusion involving NEK11 has unknown clinical significance but warrants further biological validation and could potentially lead to the development of a novel therapeutic target. Finally, the STB discussed outlier expression of a Polo-like kinase for Patient 2. Polo-like kinases regulate the transition from G2 to M phase, and are being targeted as a class due to their ubiquitous expression in cancer(*4*).

## Patient 4, Metastatic melanoma, Results

Patient 4 is a 48-year-old woman diagnosed with metastatic melanoma who underwent wide local excision for ulcerated Spitzoid-type melanoma on her right heel (**Figure S5**). One of two sentinel lymph nodes was positive leading to a right inguinal femoral lymph node dissection. She elected observation but subsequently developed diffuse skin recurrences on her right leg and was enrolled in the MI-ONCOSEQ study. She had four skin punch biopsies and confirmed that 3 of 4 had tumor content greater than 75-80%. We completed integrative sequencing and analysis for presentation in STB within 24 days of biopsy.

Tumor analyses identified 36 non-synonymous point mutations, 269 CNAs, 158 rearrangements, and 4 gene fusions (**Supplementary Tables**). Of these, the following were nominated for presentation to the STB: an activating mutation of H-ras (Q61L), a point mutation in the ETS transcription factor family member Elk-1 (R74C), and a complex rearrangement abolishing the open reading frame of cyclin dependent kinase inhibitor 2C (CDKN2C or p18INK4C). Mutations were not observed in the prevalent melanoma oncogenes B-raf, C-kit, or N-ras(5). Copy number analysis from tumor exome and whole genome data did not reveal major amplification for genes of interest. No germline aberrations were observed corresponding to the Human Gene Mutation Database(6).

The STB deliberated on Patient 4's findings. Inactivating deletions in CDKN2C, an inhibitor of CDK4, have been reported in glioblastoma multiforme and have prognostic significance in up to 30% of multiple myeloma(7). Elk-1 was of interest since ETS transcription factors are downstream targets of a relevant signaling pathway in melanoma (Ras-MAPK) and a recent study demonstrated amplification of another ETS transcription factor oncogene (ETV1) in melanoma(8). Though biologically intriguing, the clinical relevance of Elk-1 is not known. Finally, the STB nominated H-ras as a potential target for clinical trials. The H-ras activating mutation was surprising, since H-ras mutations have not been described in malignant melanoma, whereas N-ras mutations are common (15%)(9). Constitutive Ras signaling leads to downstream activation of MAPK/MEK and PI3K/mTOR cascades and provides the biological rationale for ongoing clinical trials with inhibitors of MEK, PI3K, and mTOR (mammalian target of rapamycin) for patients with Ras activated cancers(9-12). It was also noted that this patient's tumor harbored wildtype B-raf and mutant Ras. Based on findings that inhibitors of mutant B-raf can paradoxically activate MAPK signaling, this genotype combination could become relevant to outcomes for B-raf or MEK inhibitors in a clinical trial(13). This patient could potentially qualify for an upcoming trial involving combined treatment with PI3K and MEK inhibitors for specified solid tumor malignancies with K-ras, N-ras, and B-raf mutations (NCT01363232).

## II. Supplementary Methods

### Study Design

#### Flexible default informed consent

Despite the promise of clinical sequencing, there are no evidence-based guidelines to direct how informed consent for genomic sequencing and disclosure of results should be conducted(14). Incidental findings could include risk for conditions with a heritable component (e.g., hemochromatosis). An effective consent process must respect patient autonomy, address the potential impact of incidental findings, and optimize the physician's ability to provide effective treatment. We developed a consent strategy termed "flexible default consent" that accommodates all of these priorities. Findings that directly impact the current management of one's cancer could be disclosed by "default". Patients have the "flexibility" to decline incidental findings – results that do not pertain to the clinical management of their cancer – at time of consent. This consent allows a patient to focus on their current clinical care and avoid the burden

of potentially unrelated information. Due to these complexities, we believe that up-front genetic counseling is necessary to make these decisions, as incidental findings may contain clinically relevant information for patients and their families. As the study moves forward, we are collecting data on both patient and clinician attitudes through interviews and surveys to empirically assess the merits of this consent and revise the protocol if necessary.

## Sample Processing Overview

Nucleic acids were prepared from tumor and normal tissues using standard commercially available kits as described below. RNA integrity was confirmed by an Agilent Bioanalyzer. A board-certified pathologist (L.P.K.) evaluated histologic sections for tumor content. In general, tumor content exceeded 60%. We generated whole genome and transcriptome libraries for tumors according to Illumina protocols. Exome capture was performed for tumor and germline DNA with SureSelect Human Exon Target Enrichment kit (Version 2, Agilent)(Patient 1-2) or NimbleGen Sequence Capture kits (Roche)(Patient 3-4). Each library was sequenced on one lane of an Illumina HiSeq 2000. The entire process was completed within a clinically relevant timeframe of four weeks to allow time for CLIA-validation of selected findings. For the exploratory study, high-throughput sequencing was not performed in a CLIA-certified lab, and therefore any findings that could be used for clinical decision-making would require separate CLIA-certified validation. The exploratory study is accumulating data to facilitate the CLIA-certification of high-throughput sequencing for a defined set of genetic aberrations.

## Sample and sequencing library preparation

Frozen tissue samples were taken from OCT-embedded, flash frozen tissue biopsies. Total RNA was extracted from tumor tissues using Trizol reagent (Invitrogen) with mechanical disruption using a TissueLyzer II (Qiagen) with 5 mm stainless steel beads. Following precipitation with isopropanol, the RNA pellet was resuspended in Trizol and extracted again to remove any remaining genomic DNA. The quality of RNA was assessed with the Agilent Bioanalyzer 2100 using RNA Nano reagents (Agilent). Two rounds of poly(A) selection were performed using Sera-Mag oligo(dT) magnetic beads (Thermo) following the Illumina protocol starting with 1 mg total RNA. Transcriptome libraries from the mRNA fractions were generated following the RNA-SEQ protocol (Illumina) using paired-end adapters, and size selected using 3% NuSieve agarose gels (Lonza) followed by gel extraction using QIAEX II reagents (Qiagen) with a gel melting temperature of 32° C. Libraries were quantified using the Bioanalyzer 2100 using the DNA 1000 protocol and reagents (Agilent). Each sample was sequenced in a single lane with the Illumina HiSeq 2000 (100 nucleotide read length).

Genomic DNA was isolated using the Qiagen DNeasy Blood & Tissue Kit according to the manufacturer's instructions. Briefly, tissue specimens were incubated at 65° C in the presence of proteinase K and SDS, purified on silica membrane-based mini-columns, and eluted in buffer AE (10 mM Tris-HCl, 0.5 mM EDTA pH 9.0).

Exome libraries of matched pairs of tumor / normal genomic DNAs were generated using the Illumina Paired-End Genomic DNA Sample Prep Kit, following the manufacturers' instructions. 1.5 µg of each genomic DNA was sheared using a Covaris S2 to a peak target size of 250 bp. Fragmented DNA was concentrated using AMPure XP beads (Beckman Coulter), and DNA ends were repaired using T4 DNA polymerase, Klenow polymerase, and T4 polynucleotide kinase. 3' A-tailing with exo-minus Klenow polymerase was followed by ligation of Illumina paired-end adapters to the genomic DNA fragments. The adapter-ligated libraries were electrophoresed on 3% Nusieve 3:1 (Lonza) agarose gels and fragments between 300 to 350 bp were recovered using QIAEX II gel extraction reagents (Qiagen). Recovered DNA was

then amplified using Illumina PE1.0 and PE2.0 primers for 9 cycles. The amplified libraries were purified using AMPure XP beads and the DNA concentration was determined using a Nanodrop spectrophotometer. 1 mg of the libraries were hybridized to the Agilent biotinylated SureSelect Capture Library at 65°C for 72 hr or to the Roche EZ Exome capture library at 47°C for 72 hr following the manufacturer's protocol. The targeted exon fragments were captured on Dynal M-280 streptavidin beads (Invitrogen), washed, eluted, and enriched by amplification with the Illumina PE1.0 / PE2.0 primers for 8 additional cycles. After purification of the PCR products with AMPure XP beads, the quality and quantity of the resulting exome libraries were analyzed using an Agilent Bioanalyzer.

Genomic libraries of tumor DNAs were generated using the Illumina Paired-End Genomic DNA Sample Prep Kit, following the manufacturers' instructions. 1.5 µg of each genomic DNA was sheared using a Covaris S2 to a peak target size of 500 bp. Fragmented DNA was concentrated using AMPure XP beads (Beckman Coulter), and DNA ends were repaired using T4 DNA polymerase, Klenow polymerase, and T4 polynucleotide kinase. 3' A-tailing with exo-minus Klenow polymerase was followed by ligation of Illumina paired-end adapters to the genomic DNA fragments. The adapter-ligated libraries were electrophoresed on 3% Nusieve 3:1 (Lonza) agarose gels and fragments between 600 to 700 bp were recovered using QIAEX II gel extraction reagents (Qiagen). Recovered DNA was then amplified using Illumina PE1.0 and PE2.0 primers for 8 cycles. After purification of the PCR products with AMPure XP beads, the quality and quantity of the resulting genome libraries were analyzed using an Agilent Bioanalyzer and DNA 1000 reagents.

### Sequencing quality control

We used the publicly available software FastQC (<http://www.bioinformatics.bbsrc.ac.uk/projects/fastqc/>) to assess sequence quality. For each lane, we examine per-base quality scores across the length of the reads. Lanes were deemed passing if the per-base quality score boxplot indicated that >75% of the reads had >Q20 for bases 1-80. All lanes passed this threshold. Variability in the base quality at the low quality end of the reads was observed. This behavior is typical of recent HiSeq 2000 runs. In addition to the raw sequence quality, we also assess alignment quality using the Picard package. This allows monitoring of duplication rates and chimeric reads that may result from ligation artifacts; crucial statistics for interpreting the results of copy number and structural variant analysis.

### Sanger sequencing to validate novel somatic point mutations

Somatic point mutations and indels nominated by the Sequencing Tumor Board were amplified and sequenced for validation. Briefly, fifty nanograms of DNA were used as template in PCR amplifications with Hot-Start Taq DNA polymerase (Qiagen) with the suggested initial denaturation and cycling conditions. Primer sequences are listed below. The PCR products were subjected to Sanger sequencing by the University of Michigan DNA Sequencing Core after treatment with ExoSAP-IT (GE Healthcare) and sequences were analyzed using Sequencher 4.10.1 software (GeneCodes).

BRAF_15_F	GTAAAACGACGCCAGTTTGTGAATACTGGAACTATGAAA
BRAF_15_R	TCATCCTAACACATTCAAGCC
TP53_4_F	GTAAAACGACGCCAGTGGCCAGACCTAAGAGCAATC
TP53_4_R	AAGCTCCTGAGGTGTAGACGC
HRAS_2_F	GACATGCGCAGAGAGGACAG
HRAS_2_R	GTAAAACGACGCCAGTGAGAGGCTGGCTGTGAAC
NRAS_2_F	AAAGCTCTATCTCCCTAGTGTGGTA

NRAS\_2\_R

GTAAAACGACGCCAGTGGCAGAAATGGGCTTGAATAG

## Bioinformatics Overview

### Somatic and germline point mutation identification from exome sequencing

All captured libraries were sequenced using the Illumina HiSeq 2000 in paired-end mode, yielding at least 100 base pairs from the final library fragments. The reads that passed the chastity filter of Illumina base calling software were used for subsequent analysis. For the pilot project, variant calling was performed redundantly using two separate analysis pipelines with the intention of assessing and maximizing overall accuracy. The pipelines used different versions of the human reference genome (NCBI36/hg18 and NCBI GRCh37/hg19) and different read mapping tools (Bowtie(15) and BWA(16)). Further, the first pipeline (referred to below as the “Bowtie/in-house pipeline”) incorporated a set of heuristic filters developed in-house and vetted on a panel of validated mutations in human cancer tissues and cell lines (Grasso *et al.*, In submission). The second (referred to below as the “BWA/GATK pipeline”) employed the Genome Analysis Toolkit (GATK)(17) for both variant and indel calling. Finally, the variant calls from the two pipelines were merged. For the pilot project, we aimed for maximum sensitivity to detect somatic mutations and therefore considered the union of the variant calls from both pipelines. The details of the current approaches are discussed below.

#### Bowtie/In-house somatic variant calling pipeline

Mate pairs were pooled and then mapped as single reads to the reference human genome (NCBI build 36.1, hg18) using Bowtie version 0.12.5. Only the standard human chromosomes 1-22, X, Y, and mitochondrial DNA were considered. Only uniquely mapping reads with 2 or fewer mismatches were kept. We removed reads that had the same matching alignment interval that likely represent PCR duplicates. Individual base calls with Phred quality less than Q20 were excluded from further consideration. A mismatched base (SNV) was identified as a somatic mutation only when 1) it had at least six reads of support, 2) it was in at least 10% of the coverage at that position in the tumor, 3) it was observed on both strands, and 4) it did not occur in the matched normal sample in more than two reads and 2% of the coverage. SNVs were excluded from further consideration as somatic mutations if 1) they did not fall within an Agilent SureSelect or Roche NimbleGen pulldown region, or 2) they were present in dbSNP132.

Indel calling in the Bowtie/in-house pipeline was adapted with minor modifications(18). Reads for which Bowtie was unsuccessful in identifying an ungapped alignment were converted to FASTA format and mapped to the exome capture kit’s pulldown regions, padded by 200 bases on either side, with cross\_match (v0.990329, <http://www.phrap.org>), using parameters –gap\_ext -1 –bandwidth 10 –minmatch 20 –maxmatch 24. Output options were –tags –discrep\_lists –alignments. Alignments with an indel were then filtered for those that: 1) had a score at least 40 more than the next best alignment, 2) mapped at least 75 bases of the read, and 3) had two or fewer substitutions in addition to the indel. Reads from filtered alignments that mapped to the negative strand were then reverse-complemented and, together with the rest of the filtered reads, remapped with cross\_match using the same parameters (to reduce ambiguity in called indel positions due to different read orientations). After the second mapping, alignments were re-filtered using criteria 1-3. Reads that had redundant start sites were removed as likely PCR duplicates, after which the number of reads mapping to either the reference or the non-reference allele was counted for each. An indel was called if there were at least six non-reference allele reads making up at least 10% of all reads at that genomic position. Indels were reported with respect to genomic coordinates. For insertions, the position reported was the last base before the

insertion. For deletions, the position reported was the first deleted base. Indel somatic mutation candidates were excluded from further consideration if 1) they did not fall within an Agilent SureSelect pulldown region, 2) they were present in dbSNP132, or 3) they occurred in a single read in any normal exome sample.

### **GATK variant calling pipeline**

Paired-end reads were aligned to the human reference genome (hg19, standard chromosomes 1-22, X, Y, and mitochondrial DNA) using BWA v0.5.9 and allowing up to two mismatched bases per read. We performed base quality recalibration, realignment around known indels, and removal of duplicate alignments using various packages in GATK(17), Samtools(19), and Picard. The GATK UnifiedGenotyper and IndelGenotyper V2 were used to call SNVs and indels in both the tumor and normal samples with the following parameters: standard call confidence=50, standard emission confidence=10, trigger call confidence=45, minimum base quality=30, minimum read quality=20, and default values for all other parameters.

Tumor-specific variants were excluded from further consideration as somatic mutations if 1) they were called in the corresponding normal sample, 2) they did not fall within an exome kit (Agilent SureSelect or Roche EZ Exome) pulldown region, or 3) they were present in dbSNP132. Germline variants were called whenever 1) there were at least 8 reads supporting the variant, 2) at least 10% of the coverage at that position supported the variant, 3) reads supporting the variant aligned to both DNA strands, and 4) the variant position were not already present in dbSNP132.

### **Annotation of point mutation calls**

All somatic and germline mutation candidates were annotated with respect to their ability to produce non-synonymous changes and their potential effect on protein structure. Variants were annotated using dbSNP132, HapMap 3, the Catalogue of Somatic Mutations in Cancer (COSMIC) database(20,21), and the Human Gene Mutation Database (HMGD)(6).

### **Structural rearrangements and copy number alteration detection from whole genome sequencing**

Paired-end sequencing reads were aligned to the human reference genome version hg18 using BWA 0.5.9. Alignments were processed to remove duplicate reads using Picard 1.38. Breakdancer version 1.1 was used to discover structural variation in each sequenced sample from this set of duplicate-removed reads(22). Structural variant candidates were filtered for size and quality. Copy number variation was assessed using the ReadDepth 0.9.8.1 package within R 2.10.1 using the aligned set of reads without duplicates removed(23).

Common germline copy number and structural polymorphisms were derived from a three normal genomes from matched normal tissues including Patient 1, 2, and a third prostate cancer specimen. This set of variants was subtracted from tumor copy number and structural variant calls. For tumor samples derived from xenografts we performed the copy number and structural variation calling process separately against human and mouse reference genomes, and then subtracted any events common to both human and mouse.

### **Copy number alteration detection from exome sequencing**

In order to infer copy number changes by exome capture sequencing, we compared each exon's coverage in the tumor sample against its corresponding coverage in the matched normal sample. Those exons with fewer than 10 reads (850 base pairs) of coverage in the matched

normal sample, as well as those exons on the Y chromosome, were excluded from analysis. For each of the remaining exons, after adding a small positive constant (850 base pairs of coverage) to the raw coverage values in both tumor and matched normal samples, we divided these modified coverage values by the total number of human mappings in the corresponding sample, thereby accounting for variation in sequencing depth. The resulting value for the tumor sample was then divided by the resulting value for the matched normal sample and subsequently log-transformed (base 2). These log-transformed normalized coverage ratios were median centered and used for downstream segmentation analysis.

Segmentation analysis was performed through the CBS Algorithm(24) as implemented in the DNAcopy package in R (R package version 1.22.1, [www.R-project.org](http://www.R-project.org)). Default values for all parameters were used, except that consecutive segments were merged using the undo.splits="sdudo" option with the undo.SD parameter set to 0.3/DLRS, where DLRS (derivative log-ratio spread) represents the local standard deviation in log-ratios, a well-known measure of variability for CGH microarrays. In this way, the segmentation algorithm was tuned to detect copy number changes of at least 0.3 in magnitude on the log2 scale. Segments were reported as amplified or deleted if the corresponding estimated copy number ratio was greater than 1.3 or less than 0.7, respectively.

### Tumor content estimation from exome sequencing data

Tumor content was estimated for each cancer sample by fitting a binomial mixture model with two components to the set of most likely SNV candidates on 2-copy genomic regions. The set of candidates used for estimation consisted of coding variants that 1) exhibited at least  $\geq 3$  variant fragments in the cancer sample, 2) exhibited zero variant fragments in the matched benign sample with at least 16 fragments of coverage, 3) were not present in dbSNP131, 4) were within a SureSelect exon or within 100 base pairs of a SureSelect exon, 5) did not result in the extension of a homopolymer run consisting of four or more bases and 6) exhibited no evidence of amplification or deletion.

In order to filter out regions of amplification or deletion (criterion 6), we used normalized exon capture coverage data to infer copy number changes. Specifically, for each cancer sample and SureSelect exon, we computed normalized coverage as total coverage per million mapped reads, and divided this by the corresponding quantity in the matched normal sample. The resulting data was log-transformed (base 2) and segmented into regions of equal relative copy number via the Circular Binary Segmentation algorithm as implemented in the R package DNAcopy, version 1.22.1. Resulting SNV candidates were eliminated if the segmented log-ratio exceeded 0.25 in absolute value. Candidates on the X and Y chromosome were also eliminated because they were unlikely to exist in 2-copy genomic regions.

Using this set of candidates, we fit a binomial mixture model with two components using the R package flexmix, version 2.2-8. One component consisted of SNV candidates with very low variant fractions, presumably resulting from recurrent sequencing errors and other artifacts. The other component, consisting of the likely set of true SNVs, was informative of tumor content in the cancer sample. Specifically, under the assumption that most of the observed SNV candidates in this component are heterozygous SNVs, we expect the estimated binomial proportion of this component to represent one-half of the proportion of tumor cells in the sample. Thus, the estimated binomial proportion as obtained from the mixture model was doubled to obtain an estimate of tumor content in each sample.

### Gene fusion discovery from RNA-Seq

We have adapted and refined our approach to achieve accurate gene fusion discovery from RNA-Seq data(25,26). A software tool, called ChimeraScan, is now publicly available and currently under review by the journal Bioinformatics (<http://chimerascan.googlecode.com>). Improvements over the version from Maher et al. include the ability to process long (>75bp) paired-end reads, sensitive handling of ambiguously mapping reads that participate in gene fusions, detection of fusion breakpoint spanning reads, and integration with the Bowtie aligner and SAM alignment format.

Candidate gene fusions nominated by ChimeraScan were manually examined for fidelity. Reads supporting the fusion were realigned using BLAT (UCSC Genome Browser) to reconfirm the fusion breakpoint. The sequence of the fusion gene was analyzed using an NCBI tool for open reading frame (ORF) analysis (<http://www.ncbi.nlm.nih.gov/gorf/gorf.html>). For fusions with robust ORFs, the amino acid sequences of the fused proteins were explored using the UniProt database (<http://www.uniprot.org/>) to examine the gain or loss of known functional domains.

### **Outlier analysis from RNA-Seq**

Genes were nominated as exhibiting potential “outlier” expression relative to a cohort of previously sequenced tissues and cell lines using the following conditions: (1) the gene was required to have an expression value of at least 20 RPKM in the sample of interest; (2) the gene was required to be at or above the 90th percentile relative to all previously sequenced tissues, of any type; (3) the gene was required to have a fold change of at least 2 relative to the maximum RPKM over all previously sequenced benign tissues; and (4) the 25<sup>th</sup> percentile of the gene expression measurements over the previously sequenced tissues was required to be less than 50 RPKM. Collectively, these conditions target genes with (1) high absolute expression, (2) high expression relative to previously sequenced tissues, (3) high expression relative to all benign tissues, and (4) expression that is not uniformly high across all tissues. Furthermore, for the two xenografts, the colon sample, and the melanoma sample, we required, as an additional filter, that the median RPKM across tissues and cell lines of the same tissue type (prostate, prostate, colon, and melanoma, respectively), be less than 20 RPKM, to rule out genes with tissue-specific high expression.

### **Integration of multiple sequencing modalities**

Partially redundant sequencing of areas of the genome affords the ability for cross validation of findings. We cross-validated exome-based point mutation calls by manually examining the genomic and transcriptomic reads covering the mutation using the UCSC Genome Browser. Currently we do not cross-validate indel candidates as our transcriptome alignment steps utilize Bowtie, which is not capable of gapped alignment.

## **III. Supplementary Discussion**

### **Sequencing strategies**

The ability to characterize the sensitivity and specificity of high-throughput sequencing to detect clinically significant mutations remains a major challenge. To justify our approach, we performed a limit study of the sensitivity of high-throughput sequencing. We downloaded the point mutation component COSMIC database version 54, and extracted a set of 5,944 nucleotide positions, omitting long indels (>10bp) from consideration. We then quantified the depth of coverage at these positions in all data sets using BEDTools (**Figure S8**)(27). For all patients, the exome sequencing data achieved high coverage of COSMIC mutations, with >90% of mutations

covered at greater than or equal to 8X (a threshold used in some previous studies)(18). Thus, we estimate the upper bound in sensitivity for exome sequencing and variant calling at >90%. The remaining 10% lack sufficient coverage to make a reliable variant call. Of the three sequencing modalities, exome sequencing has a clear advantage for calling point mutations in COSMIC mutations in protein coding genes. However, as we have shown in this study transcriptome data can frequently provide strong supporting evidence for a particular mutation. Shallow whole genome sequencing does not appear to be of substantial benefit for point mutation calling; however, one can expect to see a handful of supporting genomic reads for any given COSMIC mutation. Combining all three data sets together prior to variant calling remains a distinct possibility, though recent reports of widespread incongruences between DNA and RNA sequencing may introduce errors in practice(28). Such an integrative variant caller should therefore accommodate the possibility of RNA editing into its methodology.

In this pilot study, we noted that our whole genome sequencing data sets had less coverage than originally planned, leading to a lack of sensitivity and specificity for structural rearrangement calls. Therefore, though whole genome sequencing data provided ancillary support for certain gene fusion calls, we relied primarily upon the RNA-Seq data in this pilot project. As we incorporate the latest sequencing technologies, we anticipate that the higher coverage will enable sensitive and specific calls.

### Bioinformatics strategies

We believe that the bioinformatics strategies employed here represent a reasonable first step in the context of our pilot project. As a next step, we anticipate that the bioinformatics community will need to define the parameters and quality controls required to move high-throughput sequencing towards CLIA-certification. To this end, we plan to continuously reevaluate our mutation calling strategies by benchmarking new methods against growing lists of true and false positive mutation lists. Further, many new software packages are being developed and released into the public domain. For example, MuTect (an extension of the Genome Analysis Toolkit, <http://www.broadinstitute.org/gsa/wiki/index.php/MuTect>), VarScan(29) (<http://varscan.sourceforge.net/>), and SomaticSniper (<http://genome.wustl.edu/software/somaticsniper>) could be promising tools for clinical bioinformatics. In the gene fusion calling domain, deFuse (<http://defuse.sf.net>) has produced excellent results in cancer studies, and newer tools now enable the *de novo* discovery of gene fusions without the need for a reference genome(30,31). We also plan to assess integrative tools such as Comrad (<http://fusioncomrad.sf.net>) for making gene fusion calls in conjunction with structural variation calling(32). For gene expression quantification, the Cufflinks package has reached stability and has been shown to yield precise transcript abundance estimates and can disambiguate transcript isoforms(33). These examples are just a small subsampling of the already large and growing bioinformatics software space. Tools such as these will need to be rigorously evaluated and tested before being deployed for use in clinical sequencing efforts. As our MI-ONCOSEQ study moves from a pilot phase into production, we expect to formalize benchmarking efforts and work with clinical sequencing community to establish standardized methods. Such standardization efforts will necessarily involve simulations as well as data from well-characterized cell lines and tissues.

Large-scale clinical sequencing will also benefit from extensive quality control practices, including bioinformatics approaches for ensuring sample identity and assessing levels of contamination. To this end, we plan to add a contamination assessment tool called PathSeq (<http://www.broadinstitute.org/software/pathseq/>) to our sequencing pipelines, and expect that this increases confidence in the results(34). Furthermore, we will “fingerprint” each sample by tabulating SNP positions across the genome, and use these SNP fingerprints to track samples and ensure their identity at various stages of the analysis. These bioinformatics approaches will help solidify high-throughput sequencing as a reliable assay for clinical use.

## **Updating variant stratification for clinically relevant genes**

Over the course of the study, genes may be newly implicated as a target or informative variant in cancer. The predetermined gene lists will be updated at least every month and existing sequencing data will be queried for any new findings. If positive results are identified, these cases can be represented at STB for review of these additional findings. Disclosure will depend upon the patient's informed consent selection.

## **Costs associated with integrative high-throughput sequencing**

The breakdown of costs associated with integrative sequencing is described in **Table S1**. Thus, it will cost \$5395/patient for supplies only and \$6137/patient when computation and labor is included. As is apparent, a large percentage of the cost comes from Illumina flow cells (65%) and exome capture libraries (24%). We predict that costs will continue to decrease in the future and the majority of resources would focus on data analysis and interpretation (**Figure S9**).

Although the cost already is comparable to routine clinical tests such as OncotypeDx, we predict that the cost of integrative sequencing will decrease to the point where it could be deployed as correlative research for every patient entering a clinical trial. For example, with a single HiSeq2000 instrument, one could complete integrative sequencing for 16 patients per month to support a phase 1 clinical trial unit (2 flow channels per patient with 2 full sequencing runs per month). Based on the latest improvements in sequencing throughput (**Figure S9 and Table S2**), we now anticipate sequencing using just two lanes per patient: one lane of tumor whole genome (12-15X coverage) and one lane of multiplexed (bar-coded) tumor transcriptome, tumor exome, and constitutional exome. This strategy will reduce the cost of integrative sequencing to \$3600 per patient for reagents alone (Supplement). This is directly comparable to clinically available testing such as Oncotype Dx<sup>(35,36)</sup> (\$4075) and TargetNow<sup>(37,38)</sup> (\$3600) which are covered by Medicare and some private insurance.

## **Limitations of integrative sequencing**

Currently, most methods require fresh or frozen tissue, but new protocols for assessment of formalin-fixed paraffin-embedded materials will enable integrative sequencing for countless patients who have tissues banked or collected under standard pathology protocols. All approaches are limited by polyclonal disease or poor tumor content which dilutes detection of sequence variants; however, these problems may be partially mitigated by greater depth of sequencing as throughput improves.

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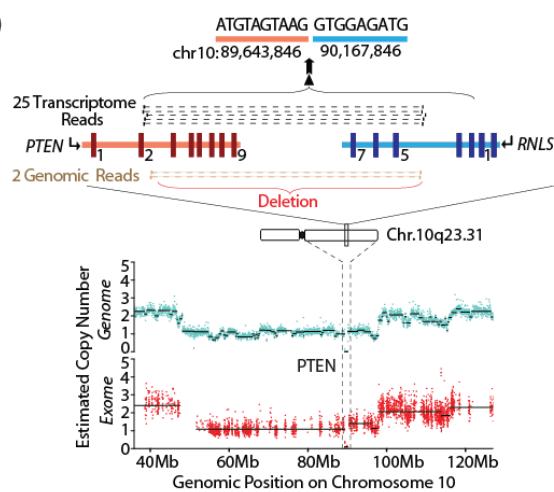
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## V. Supplementary Figures and Legends

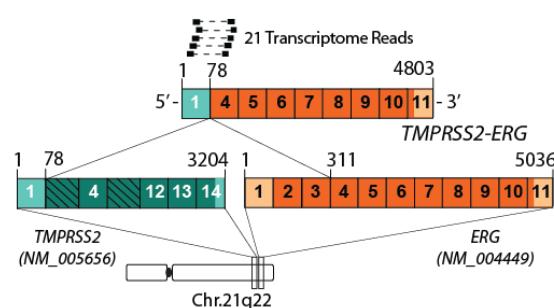
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Gene	Point Mutation	Est. Copy Number	Structure	Gene Expression
TP53	p.C141Y	1.04 (1 copy loss)		
PTEN		0.1 (2 copy loss)		Low
AR		8.5 (amplification)		
ERG			Fusion with TMPRSS2	High
NEK11			Fusion with CPNE4	High

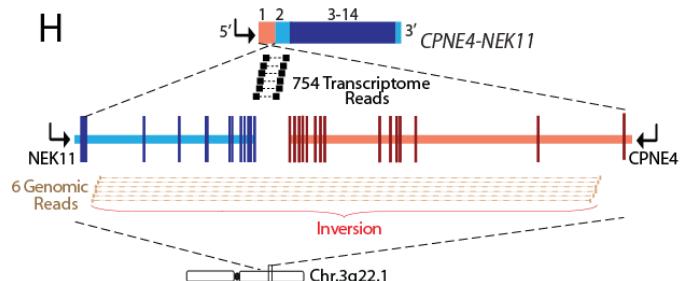
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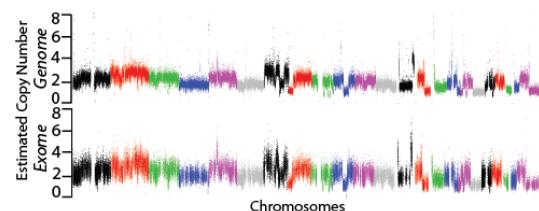
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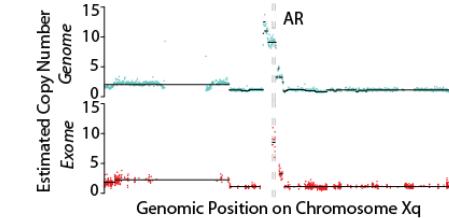
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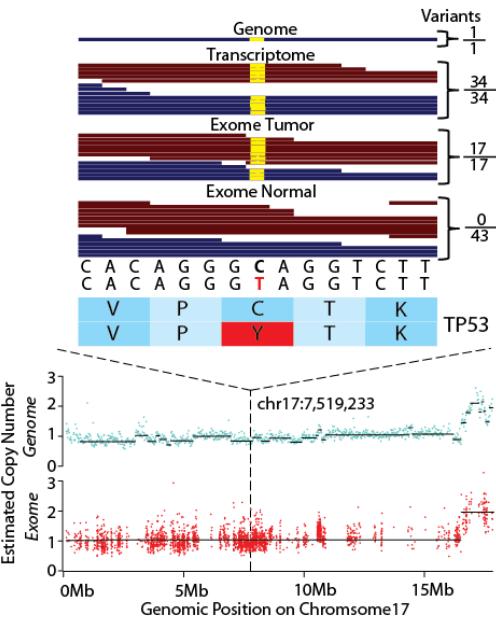
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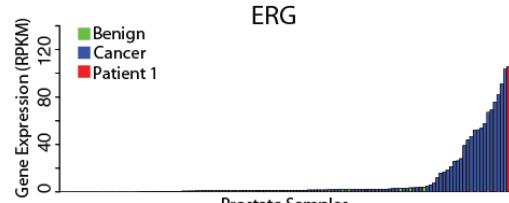
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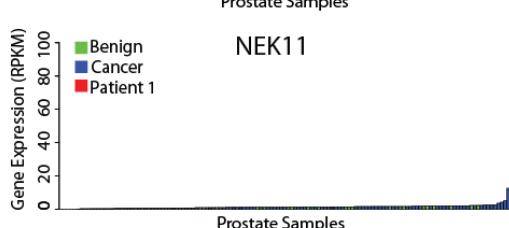
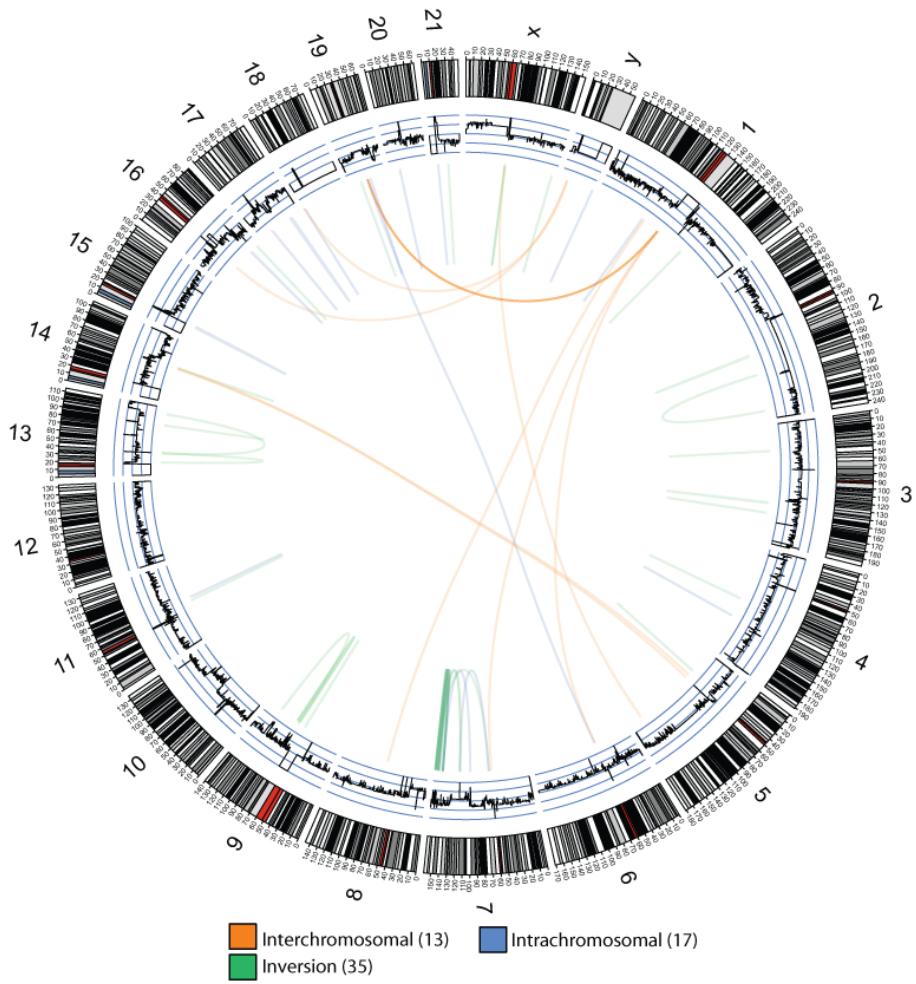
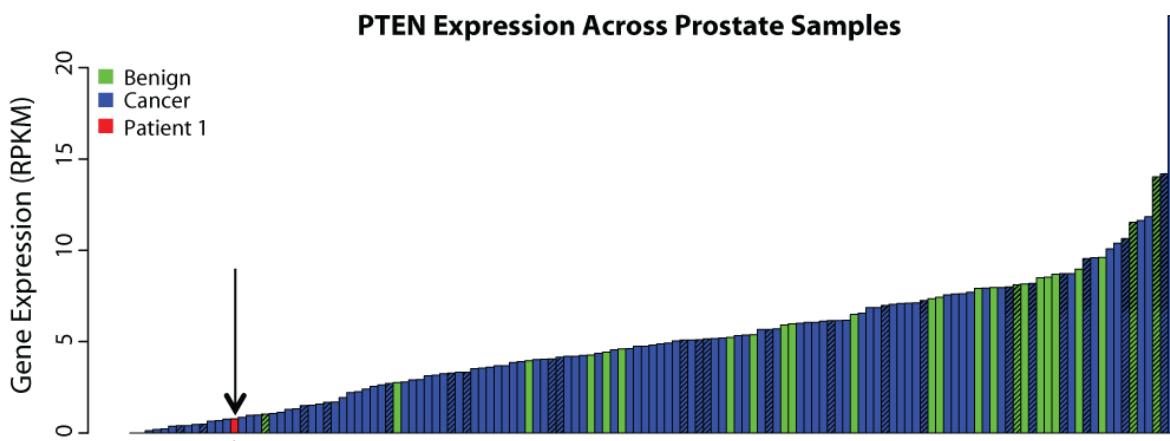


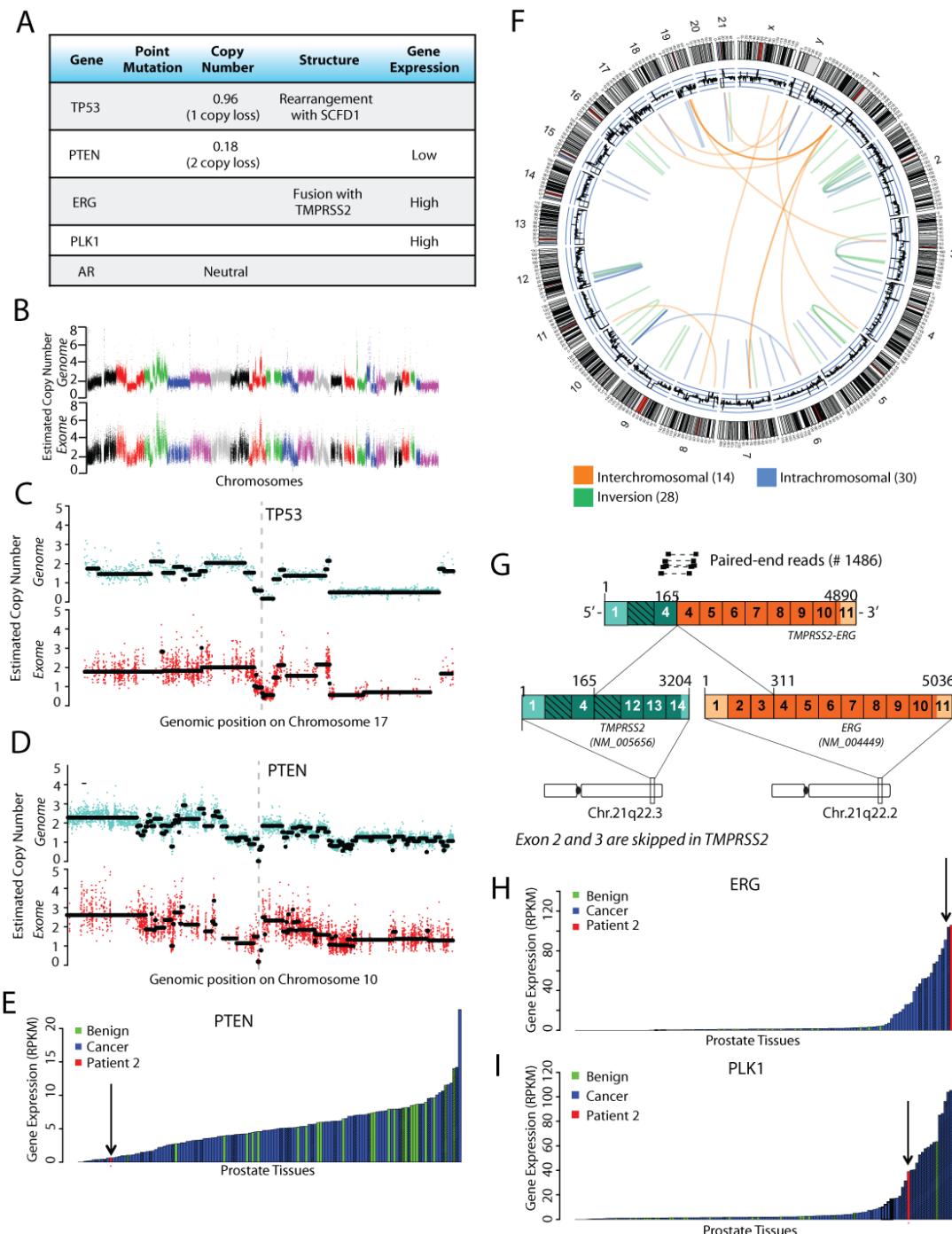
Figure S1: Integrative sequencing of a patient's prostate cancer xenograft

**Figure 1. Integrative sequencing of a patient's prostate cancer xenograft.** This is a representative example of a patient sample that was assessed in the pilot phase of this study with an additional patient represented in the Supplementary Materials. Patient 1 is a 67-year-old man with metastatic castrate-resistant prostate cancer. This patient's tumor was grown as a xenograft

in an immunodeficient mouse, and a sample of which was submitted for pilot integrative sequencing. **A**, Summary of somatic genetic aberrations identified including an inactivating mutation of TP53, homozygous loss of PTEN tumor suppressor, amplification of androgen receptor (AR), TMPRSS2-ERG gene fusion and a novel gene fusion involving the NEK11 kinase. **B**, Overall copy number analysis based on integration of exome and whole genome represented as estimated copy number. **C**, Amplification of androgen receptor (AR) is displayed as estimated copy number based on whole genome (green) and exome (orange). **D**, Homozygous loss of PTEN through deletion is displayed based on integrative assessment of whole exome and whole genome sequencing. RNA-seq also demonstrated concordant decreased expression of PTEN. **E**, A somatic inactivating point mutation (top) was detected in TP53 through integration of whole genome, transcriptome, and exome sequencing. Number of variant reads are shown for each method. Copy number analysis revealed one copy loss through integration of whole genome (green) and exome (orange) data. **F**, Rearrangement of TMPRSS2 and ERG forming a gene fusion as detected by RNA-seq. **G**, Through rearrangement with TMPRSS2, ERG is highly expressed based on RNA-seq. **H**, A novel gene fusion candidate involving an intact open reading frame for NEK11 kinase was identified based on RNA-seq and whole genome sequencing, and **I**, is highly expressed based on RNA-seq.

**A****B**

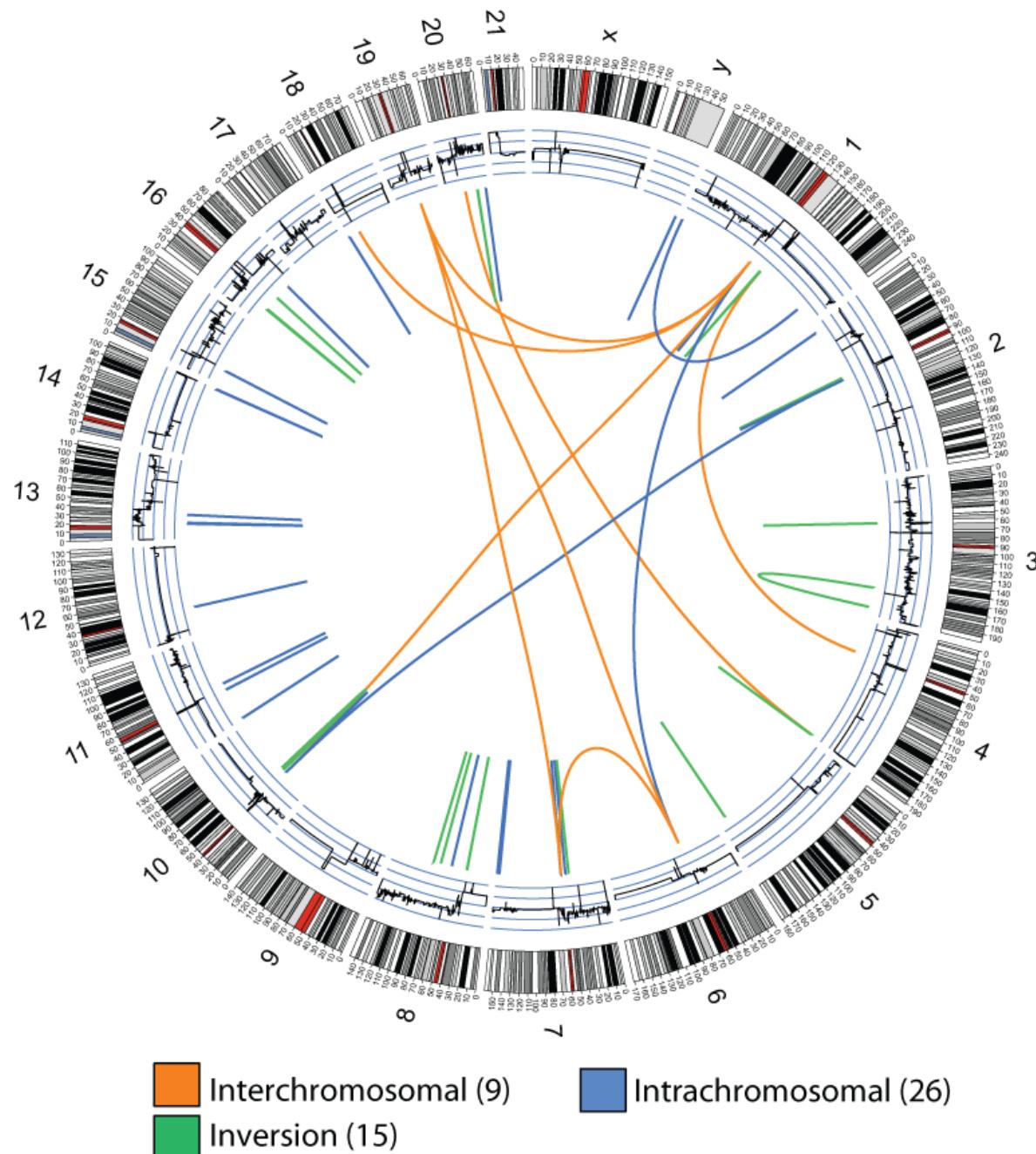
**Supplementary Figure 2: Additional aberrations reported in Patient 1 (Prostate cancer xenograft).** **A**, Circos plot derived from whole genome sequencing depicts global landscape of structural variation including deletions (green), interchromosomal (orange) and intrachromosomal (blue) rearrangements. **B**, Expression of PTEN in Patient 1 (red) is markedly decreased compared to an RNA-seq compendium of benign (green) and malignant (blue) prostate cell lines and tissues and is consistent with homozygous loss of PTEN (shown in Figure 3).



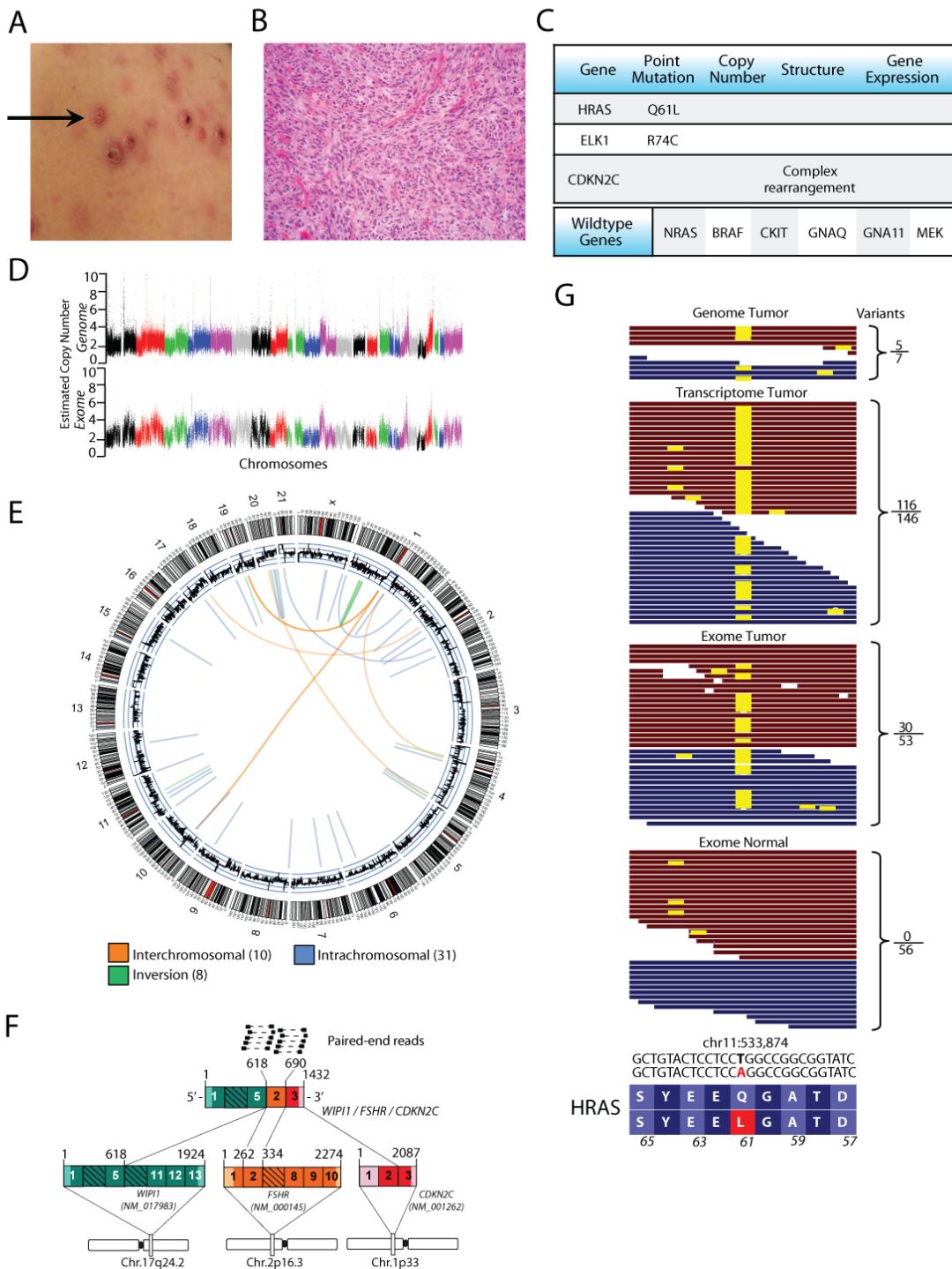
**Supplementary Figure 3: Aberrations reported in Patient 2 (Prostate cancer xenograft)**

Patient 2 is a 60-year-old man with metastatic prostate cancer. This patient's tumor was grown as a xenograft in an immunodeficient mouse, and a sample of which was submitted for pilot integrative sequencing. **A**, Summary of somatic genetic aberrations identified including an inactivating mutation of TP53, homozygous loss of PTEN tumor suppressor, and rearrangement of TMPRSS2 and ERG. **B**, Global copy number landscape derived from whole genome and exome sequencing with individual chromosomes painted. **C** and **D**, Integrated copy number analysis of whole genome (top) and exome (bottom) sequencing demonstrates (C) TP53 loss and PTEN loss (D) plotted as estimated copy number against chromosome position. **E**, Expression of PTEN in Patient 2 (red) is markedly decreased compared to an RNA-seq compendium of benign (green) and malignant (blue) prostate cell lines and tissues and is consistent with homozygous loss of PTEN. **F**, Circos plot derived from whole genome sequencing depicts global landscape of

structural variation including deletions (green), interchromosomal (orange) and intrachromosomal (blue) rearrangements. **G**, RNA-seq identified rearrangement of TMPRSS2 and ERG (an ETS transcription factor). **H**, ERG is highly expressed by RNA-seq compared to a compendium of prostate cancer. **I**, Outlier analysis of gene expression (RNA-seq) reveals Polo-like kinase 1 (PLK1) as one of the top expressed genes compared to a compendium of prostate cancer.

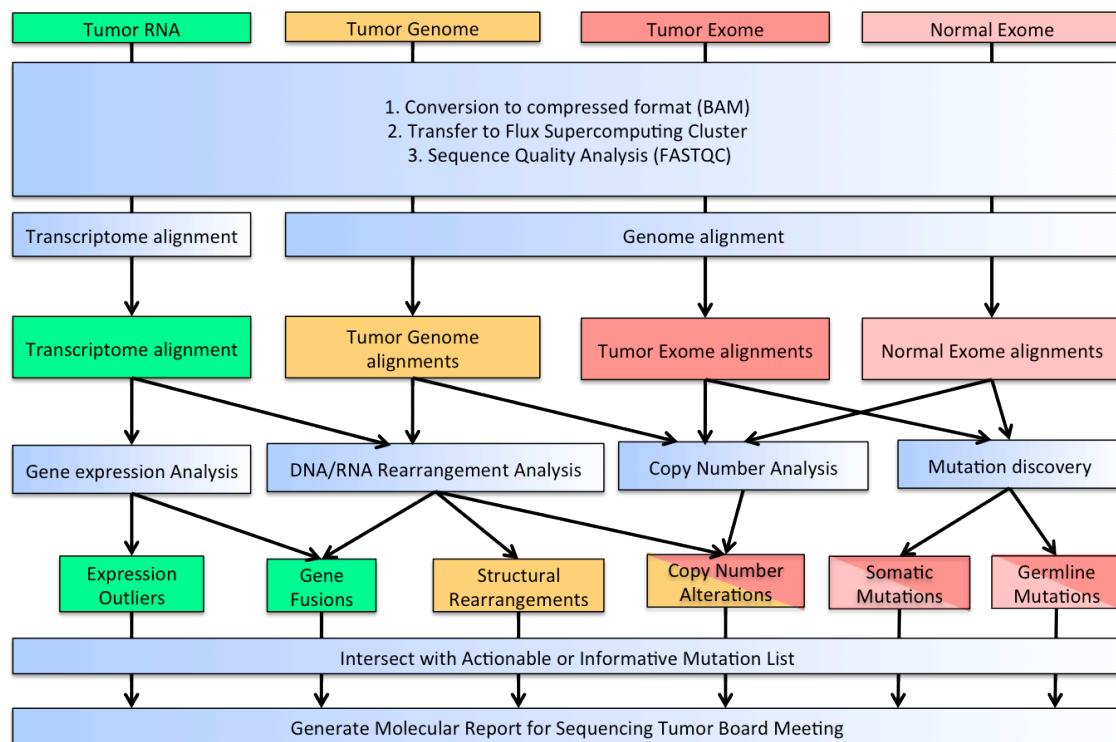


**Supplementary Figure 4: Additional aberrations reported in Patient 3 (Colorectal cancer).** Circos plot derived from whole genome sequencing depicts global landscape of structural variation including deletions (green), interchromosomal (orange) and intrachromosomal (blue) rearrangements.

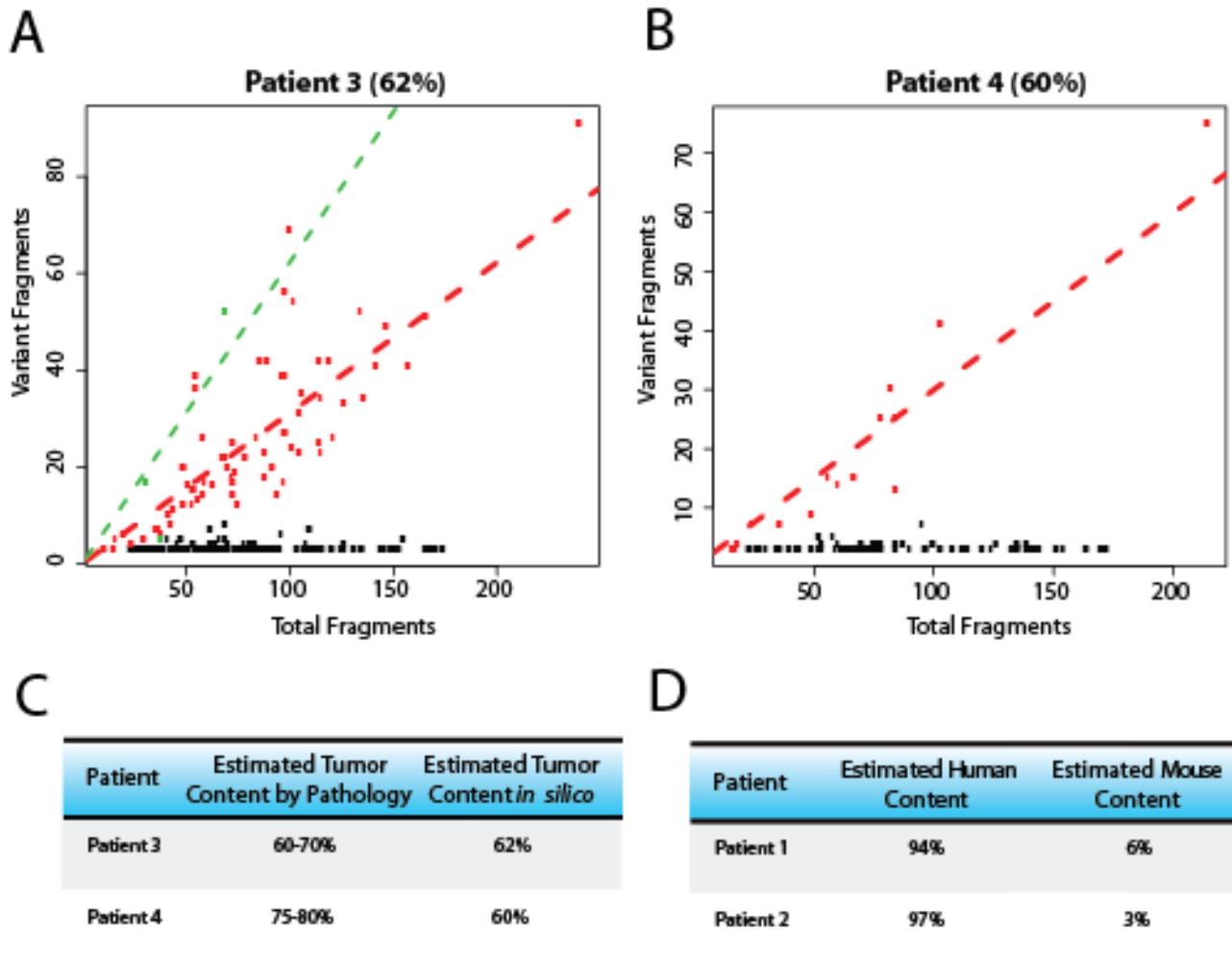


**Supplementary Figure 5: Aberrations reported in Patient 4 (Melanoma).** Patient 4 is a 48-year-old woman with melanoma diagnosed in June 2010 who had 1 of 2 positive sentinel lymph nodes, followed by a right inguinal femoral lymph node dissection. She elected for observation. Subsequently, she developed diffuse skin recurrences on her right leg up to her thigh. She was enrolled on the study for integrative sequencing. **A**, Photograph displays multiple skin metastases and sites of biopsy. **B**, Representative histology from skin biopsy demonstrates dermal proliferation of ovoid to spindle cells with frequent prominent nucleoli. **C**, Summary of mutations reveals an activating H-ras mutation (Q61L) and mutation of unknown significance in a ETS transcription factor (Elk-1). Relevant wildtype genes included B-raf, C-kit, MEK, and N-

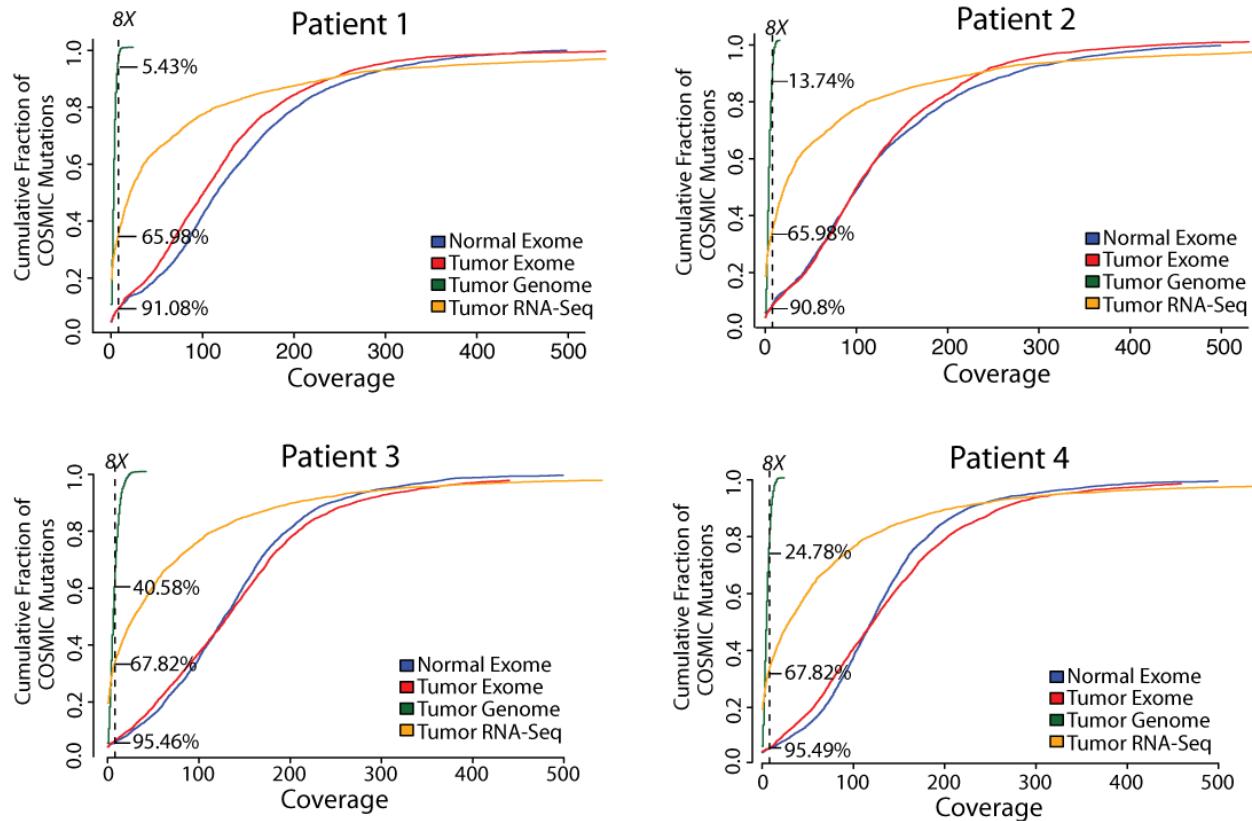
ras. Integration of exome and RNA-seq confirms H-ras mutation. **D**, Copy number landscape across chromosomes (painted different colors) derived from whole genome and exome sequencing. **E**, Circos plot derived from whole genome sequencing depicts global landscape of structural variation including deletions (green), interchromosomal (orange) and intrachromosomal (blue) rearrangements. **F**, RNA-seq data support a possible rearrangement involving CDKN2C, WIPI1, and FSHR, and is predicted to result in inactivation of CDKN2C. **G**, Integrative analysis of whole genome, transcriptome, and exome tumor sequencing provides orthogonal support for the activating H-ras (Q61L) mutation.



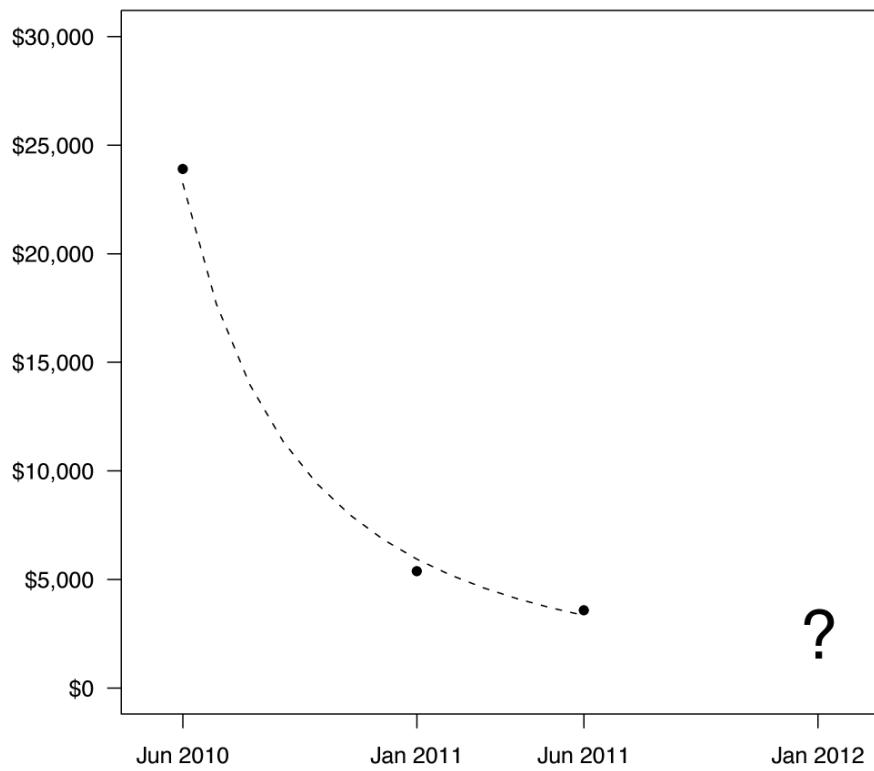
**Supplementary Figure 6: Bioinformatics workflow diagram.** DNA and RNA sequences are transferred to a high performance computer cluster and aligned to the human genome using DNA or RNA alignment strategies. Alignment results then feed into multiple analysis pipelines that produce gene expression (RPKM tabulation), gene fusions (ChimeraScan), structural rearrangement (BreakDancer pipeline), copy number alterations (ReadDepth and customized exome copy number assessment), and point mutations (BWA/GATK and Bowtie/in-house pipelines). The results are intersected in a gene-centric manner with a curated list of informative genes. The final results are tabulated for presentation to the Sequencing Tumor Board.



**Supplementary Figure 7: Tumor Content Estimation by Pathology and *in silico* prediction in tumor tissue from patients 3 and 4.** Somatic variants are displayed in a dot plot with number of variant fragments on y axis and total fragments on x axis. For heterozygous mutations, the expected frequency is 0.5 and demonstrated as a red dotted line. For homozygous mutations, the expected frequency is 1.0 and demonstrated as a green dotted line. Most variants are heterozygous, and these were used to estimate % tumor content based on deviation from 0.5 frequency. A, Patient 3 had an estimated tumor content of 62%, and B, Patient 4 had an estimated tumor content of 60%. C, Table shows the estimated tumor content by histologic evaluation of tumor biopsies which overestimates tumor content compared to *in silico* estimates. D, Human tumor purity in xenograft patient samples was estimated at 94% (Patient 1) and 97% (Patient 2).



**Supplementary Figure 8: Integrative sequencing coverage of COSMIC mutation positions.** Cumulative distribution plots for each patient depicting coverage depth across 5,944 nucleotide positions corresponding to point mutation and indel sites in the COSMIC database. The fraction of all mutation positions (Y axis) is plotted against the depth of coverage (X axis). Normal (blue) and tumor exome (red), tumor genome (green), and tumor transcriptome (orange) line plots are overlaid to indicate the pattern of coverage offered by each platform. The dotted vertical line indicates 8X coverage (a published threshold for variant calling) and is provided as a guide. The percentage of COSMIC mutations covered at >8X are indicated for each platform.



**Supplementary Figure 9: Projections for Cost of Integrative Sequencing.** Scatter plot illustrates estimated reagent cost of our integrated sequencing if performed in June 2010 (using previous Illumina model Genome Analyzer II), Jan 2011 (4 lanes Illumina HiSeq 2000, v2SBS), and June 2011 (2 lanes, Illumina HiSeq 2000, V3SBS with bar-coded libraries). By Jan 2012, integrative sequencing will include greater depth and lower cost.

## VI. Supplementary Tables

**Supplementary Table 1: Breakdown of costs associated with integrative sequencing**

Process	Sequencing Cost Breakdown (January 2011)	Cost/Patient	Cost/Patient (Multiplexing)
Nucleic Acid Isolation	DNA/RNA mini kits, Qiagen Blood & Tissue kits, QC Bioanalyzer RNA Nano 4/chip	\$18	\$18
Transcriptome Library Preparation	Seradyn oligodT, Superscript II, RNase H, DNA Pol I, T4 DNA Polymerase Pol1-Klenow, T4 Polynucl. Kinase, Klenow Frag, Quick Ligation Kit, dNTPs, Phusion® Polymerase, 3:1 AGAROSE 500G, Qiagen Gel Extraction Kit, AMPURE XP 60ML, PE 1.0 Primers, Adapters	\$51	\$51
Genomic and Exome Library Preparation	microTUBE w/ AFA Fiber, DNA Pol I, T4 DNA Pol, T4 Polynucl. Kinase, Klenow, Quick Ligation Kit, dNTPs, Phusion Polymerase, NuSieve AGAROSE, Gel Extraction Kit, AMPURE XP 60ML, PE1.0 Primers, ADAPTERs, Dynabeads M280 Beads, Human All Exome Capture Agilent	\$836	\$836
QC/Quantitation	Bioanalyzer DNA 1000 8/chip, QPCR 1ml Kappa	\$29	\$29
Sequencing Costs	PE Cluster Gen Kits Tru-Seq PE-401-2001, 8 lanes, 1 PhiX Control Kit v2(10 lanes), TruSeq SBS 2x100bp (4 HiSeq lanes/patient)	\$4,461	\$2,647
Computation costs	Servers, LIMS, Storage, Back-up, Security, Analysis CPU time (CAC Cluster)	\$213	\$213
Labor costs	Pathologist evaluation of slides, DNA extraction, sequencing library preparation, bioinformatician analysis	\$529	\$529
<b>Total costs per patient</b>		<b>\$6,137</b> <b>(\$5,395 supplies only)</b>	<b>\$4,322</b> <b>(\$3,581 supplies only)</b>

Area of Expertise	Participants
<b>Targeted Therapy/Trials</b>	Moshe Talpaz, M.D. Patricia LoRusso, D.O. David Smith, M.D. Harry Erba, M.D., Ph.D. Scott Schuetze, M.D., Ph.D.
<b>Breast Cancer</b>	Dan Hayes, M.D. Max Wicha, M.D.
<b>Gastrointestinal Cancer</b>	Mark Zalupski, M.D. Stephen Gruber, M.D., Ph.D.
<b>Genitourinary Cancer</b>	David Smith, M.D. Maha Hussain, M.D. Ken Pienta, M.D.
<b>Melanoma/Cutaneous</b>	Christopher Lao, M.D. Bruce Redman, D.O.
<b>Leukemia/Lymphoma</b>	Harry Erba, M.D., Ph.D. Moshe Talpaz, M.D. Mark Kaminski, M.D.
<b>Thoracic</b>	Greg Kalemkarian, M.D.
<b>Sarcoma</b>	Scott Schuetze, M.D., Ph.D.
<b>Cancer Genetics</b>	Stephen Gruber, M.D., Ph.D.
<b>Genetics and Counseling</b>	Jeffrey K. Innis, M.D., Ph.D. Wendy Uhlmann, M.S. Victoria Raymond, M.S. Jessica Everett, M.S. Jessica Long, M.S.
<b>Bioethics and Psychology</b>	J. Scott Roberts, Ph.D. Scott Y. Kim, M.D., Ph.D. Ray DeVries, Ph.D. Brian Zikmund-Fisher, Ph.D.
<b>Pathology</b>	Arul Chinnaiyan, M.D., Ph.D. L. Priya Kunju, M.D. Scott Tomlins, M.D., Ph.D.
<b>Bioinformatics</b>	Arul Chinnaiyan, M.D., Ph.D. Michigan Center for Translational Pathology
<b>Genomics</b>	Arul Chinnaiyan, M.D., Ph.D. Stephen Gruber, M.D., Ph.D. Dan Robinson, Ph.D.
<b>Ad Hoc Expertise</b>	University of Michigan Comprehensive Cancer Center Referring Physicians
<b>Table S2:</b> Sequencing Tumor Board expertise is derived from the University of Michigan's Comprehensive Cancer Center, Michigan Center for Translational Pathology, Medical School, Cancer Genetics, Department of Pathology, and School of Public Health. <i>Ad hoc</i> participants ensures that each case has well-represented expertise as needed.	

**Table S3: Informative Gene List**

Chromosome Position (hg19)	Strand	RefSeq Gene ID	Gene Symbol
chr1:1990929-1991080	+	NM_002744	PRKCZ
chr1:2494536-2495317	+	NM_003820	TNFRSF14
chr1:3350190-3355235	+	NM_022114	PRDM16
chr1:6259571-6259729	-	NM_000983	RPL22
chr1:11862887-11863236	-	NM_005957	MTHFR
chr1:16482292-16482632	-	NM_004431	EPHA2
chr1:17380392-17380715	-	NM_003000	SDHB
chr1:19062075-19062422	+	NM_001135254	PAX7
chr1:20944894-20945450	+	NM_001785	CDA
chr1:20976876-20978054	+	NM_032409	PINK1
chr1:22915313-22916162	+	NM_001006943	EPHA8
chr1:23222853-23223021	+	NM_004442	EPHB2
chr1:26448277-26452076	+	NR_026685	PDIK1L
chr1:26646611-26647064	+	NM_001803	CD52
chr1:26872292-26872576	+	NM_001006665	RPS6KA1
chr1:27101420-27101761	+	NM_139135	ARID1A
chr1:27692698-27693387	-	NM_004672	MAP3K6
chr1:27950151-27950490	-	NM_005248	FGR
chr1:32751064-32751816	+	NM_001042771	LCK
chr1:32798567-32799274	+	NM_004964	HDAC1
chr1:32829145-32829974	+	NM_052841	TSSK3
chr1:35657772-35658793	-	NM_005066	SFPQ
chr1:36769346-36771007	+	NM_005119	THRAP3
chr1:36826771-36826991	-	NM_032017	STK40
chr1:38227026-38227805	-	NM_001099439	EPHA10
chr1:40366560-40367165	-	NM_001033082	MYCL1
chr1:43788271-43788829	+	NM_005424	TIE1
chr1:43818138-43820185	+	NM_005373	MPL
chr1:45271108-45271717	+	NM_004073	PLK3
chr1:45799034-45799283	-	NM_001048174	MUTYH
chr1:45923185-45923593	-	NM_007170	TESK2
chr1:46500159-46501846	+	NM_015112	MAST2
chr1:47059734-47060002	-	NM_001135553	MKNK1
chr1:47691064-47691611	-	NM_003189	TAL1
chr1:51439514-51440359	+	NM_078626	CDKN2C
chr1:51887407-51887843	-	NM_001159969	EPS15
chr1:57173097-57181058	+	NM_006252	PRKAA2
chr1:59246412-59249835	-	NM_002228	JUN
chr1:64608037-64609102	+	NM_001083592	ROR1
chr1:65351891-65352074	-	NM_002227	JAK1
chr1:75009539-75010166	+	NM_015978	TNNI3K
chr1:84670114-84671029	+	NM_207578	PRKACB
chr1:85741928-85742637	-	NM_003921	BCL10
chr1:89298877-89301988	+	NM_006256	PKN2
chr1:91967194-91967438	+	NM_001134419	CDC7

chr1:92479712-92480035	+	NM_001726	BRDT
chr1:98164856-98165153	-	NM_000110	DPYD
chr1:110888110-110888321	+	NM_022768	RBM15
chr1:114497197-114497442	+	NM_181358	HIPK1
chr1:115053121-115053831	-	NM_015906	TRIM33
chr1:115258620-115258848	-	NM_002524	NRAS
chr1:120611897-120612326	-	NM_024408	NOTCH2
chr1:144930533-144932082	-	NM_001002811	PDE4DIP
chr1:147095592-147098065	+	NM_004326	BCL9
chr1:150814849-150814994	-	NM_001668	ARNT
chr1:153665777-153666518	+	NM_000906	NPR1
chr1:154144454-154144630	-	NM_001043352	TPM3
chr1:155160588-155160811	-	NM_002456	MUC1
chr1:155240548-155240818	-	NM_003993	CLK2
chr1:156770115-156770659	+	NM_005973	PRCC
chr1:156811822-156812035	+	NM_001007792	NTRK1
chr1:156828278-156828716	-	NM_014215	INSRR
chr1:161326416-161326680	+	NM_001035512	SDHC
chr1:161641134-161641489	+	NM_001002275	FCGR2B
chr1:162467544-162468108	+	NM_144624	UHMK1
chr1:162749851-162750297	+	NM_006182	DDR2
chr1:164815770-164821095	+	NM_002585	PBX1
chr1:169857766-169858081	-	NM_181093	SCYL3
chr1:179112017-179112274	-	NM_001168239	ABL2
chr1:182554411-182556158	-	NM_021133	RNASEL
chr1:186343959-186344507	-	NM_003292	TPR
chr1:186649320-186649609	-	NM_000963	PTGS2
chr1:198288491-198291598	+	NM_133494	NEK7
chr1:204518190-204527298	+	NM_002393	MDM4
chr1:205290475-205290933	-	NM_030952	NUAK2
chr1:205588345-205590016	-	NM_021795	ELK4
chr1:205633562-205634064	-	NM_033102	SLC45A3
chr1:206669394-206670273	+	NM_014002	IKBKE
chr1:206820682-206822592	+	NM_001004023	DYRK3
chr1:206905332-206907676	+	NM_004759	MAPKAPK2
chr1:209786079-209786307	+	NM_020439	CAMK1G
chr1:211848675-211849017	-	NM_002497	NEK2
chr1:213244297-213244433	+	NM_012424	RPS6KC1
chr1:220835103-220837849	+	NM_018650	MARK1
chr1:227300321-227300664	-	NM_003607	CDC42BPA
chr1:233518000-233520944	+	NM_032435	KIAA1804
chr1:241682840-241683135	-	NM_000143	FH
chr1:241682840-241683135	-	NM_000143	FH
chr1:243666433-243668686	-	NM_005465	AKT3
chr10:6556929-6557156	-	NM_006257	PRKCQ
chr10:8105908-8106151	+	NM_002051	GATA3
chr10:12870717-12871783	+	NM_153498	CAMK1D

chr10:22028908-22029215	+	NM_001195626	MLLT10
chr10:26500721-26501515	+	NM_017433	MYO3A
chr10:27461999-27462238	+	NM_032844	MASTL
chr10:30749584-30750811	+	NM_005204	MAP3K8
chr10:43623509-43625847	+	NM_020975	RET
chr10:49642871-49643233	+	NM_002750	MAPK8
chr10:51589174-51590784	+	NM_005437	NCOA4
chr10:54053511-54055324	+	NM_006258	PRKG1
chr10:72360069-72360738	-	NM_001083116	PRF1
chr10:75585028-75585155	-	NM_172173	CAMK2G
chr10:76788196-76792689	+	NM_012330	MYST4
chr10:88683300-88684995	+	NM_004329	BMPR1A
chr10:89724993-89728582	+	NM_000314	PTEN
chr10:101989134-101989394	-	NM_001278	CHUK
chr10:102896374-102897595	+	NM_001195517	TLX1
chr10:104161958-104162331	+	NM_001077494	NFKB2
chr10:104389772-104393264	+	NM_016169	SUFU
chr10:105785281-105787392	+	NM_014720	SLK
chr10:121214430-121215181	+	NM_005308	GRK5
chr10:123353172-123353822	-	NM_001144916	FGFR2
chr10:123353172-123353822	-	NM_001144916	FGFR2
chr10:134121025-134121527	-	NM_173575	STK32C
chr11:532580-532805	-	NM_005343	HRAS
chr11:532580-532805	-	NM_005343	HRAS
chr11:1482149-1483378	+	NM_003957	BRSK2
chr11:3062075-3062311	-	NR_036542	CARS
chr11:3781667-3781906	-	NM_005387	NUP98
chr11:4159374-4160156	+	NM_001033	RRM1
chr11:6625156-6625640	+	NM_001014795	ILK
chr11:8496177-8496663	-	NM_030906	STK33
chr11:9609945-9611363	+	NM_003390	WEE1
chr11:22644028-22647437	-	NM_022725	FANCF
chr11:32413476-32413660	-	NM_024424	WT1
chr11:33374587-33375989	+	NM_005734	HIPK3
chr11:33890841-33891421	-	NM_001142316	LMO2
chr11:44193173-44193342	+	NM_001178083	EXT2
chr11:47260300-47260819	+	NM_000107	DDB2
chr11:63670022-63670304	+	NM_001163296	MARK2
chr11:64135889-64136123	+	NM_003942	RPS6KA4
chr11:64570475-64570763	-	NM_004579	MAP4K2
chr11:64577086-64577654	-	NM_130799	MEN1
chr11:64577086-64577654	-	NM_130799	MEN1
chr11:64611831-64612091	-	NM_017525	CDC42BPG
chr11:65304406-65304649	+	NM_020680	SCYL1
chr11:65380438-65381770	-	NM_002419	MAP3K11
chr11:67052706-67054079	+	NM_001619	ADRBK1
chr11:67202409-67202929	+	NM_003952	RPS6KB2

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chr11:77103325-77103636	-	NM_001128620	PAK1
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chr11:100998114-101000594	-	NM_000926	PGR
chr11:102195141-102196143	+	NM_182962	BIRC3
chr11:108236001-108239876	+	NM_000051	ATM
chr11:108810922-108811698	+	NM_004398	DDX10
chr11:111249836-111250207	-	NM_006235	POU2AF1
chr11:111965478-111966568	+	NM_003002	SDHD
chr11:117038086-117041811	+	NM_002572	PAFAH1B2
chr11:117100042-117100622	-	NM_004716	PCSK7
chr11:118361860-118362083	+	NM_001197104	MILL
chr11:119170154-119178909	+	NM_005188	CBL
chr11:120355725-120360695	+	NM_015313	ARHGEF12
chr11:125545772-125546200	+	NM_001114121	CHEK1
chr12:498042-498670	-	NM_001042603	KDM5A
chr12:999568-999729	+	NM_018979	WNK1
chr12:4408975-4414572	+	NM_001759	CCND2
chr12:4722627-4723091	+	NM_003845	DYRK4
chr12:6787778-6787926	-	NM_001039916	ZNF384
chr12:10787115-10787335	-	NM_018423	STYK1
chr12:12043824-12048375	+	NM_001987	ETV6
chr12:14849115-14849569	-	NM_004963	GUCY2C
chr12:25368320-25368544	-	NM_033360	KRAS
chr12:25368320-25368544	-	NM_033360	KRAS
chr12:27475210-27478940	+	NM_015000	STK38L
chr12:40761395-40763136	+	NM_198578	LRRK2
chr12:44164972-44165218	+	NM_001114182	IRAK4
chr12:51213367-51214993	+	NM_005171	ATF1
chr12:52306062-52306369	+	NM_001077401	ACVRL1
chr12:52387718-52390913	+	NM_004302	ACVR1B
chr12:53823883-53824116	+	NM_001164690	AMHR2
chr12:53880680-53881262	-	NM_001193511	MAP3K12
chr12:54338733-54340378	+	NM_017410	HOXC13
chr12:54368914-54370253	+	NM_014212	HOXC11
chr12:56365254-56366618	+	NM_001798	CDK2
chr12:56478728-56479451	+	NM_001005915	ERBB3
chr12:57118185-57118383	-	NM_001113201	NACA
chr12:57911001-57911257	-	NM_001195057	DDIT3
chr12:58145232-58145569	-	NM_000075	CDK4
chr12:64895059-64895949	+	NM_013254	TBK1
chr12:65514773-65515396	-	NM_007191	WIF1
chr12:66308788-66309357	+	NM_003484	HMGAA2
chr12:66597440-66597723	+	NM_007199	IRAK3
chr12:68050835-68056494	+	NM_006482	DYRK2
chr12:69233003-69239262	+	NM_002392	MDM2

chr12:92539113-92539723	-	NM_001731	BTG1
chr12:100732255-100733964	+	NM_017988	SCYL2
chr12:106532141-106533861	-	NM_014840	NUAK1
chr12:112247296-112247834	+	NM_000690	ALDH2
chr12:112942448-112942650	+	NM_002834	PTPN11
chr12:118693202-118693510	-	NM_016281	TAOK3
chr12:119631453-119632601	+	NM_014365	HSPB8
chr12:120313826-120314035	-	NM_007174	CIT
chr12:121682325-121682468	-	NM_172214	CAMKK2
chr12:122492660-122492945	+	NM_020993	BCL7A
chr12:132405800-132407757	+	NM_003565	ULK1
chr13:21619773-21620419	-	NM_014572	LATS2
chr13:26978042-26978619	+	NM_001260	CDK8
chr13:28542552-28543367	-	NM_001265	CDX2
chr13:28674554-28674779	-	NM_004119	FLT3
chr13:28674554-28674779	-	NM_004119	FLT3
chr13:28959637-28964291	-	NM_001159920	FLT1
chr13:32972248-32973859	+	NM_000059	BRCA2
chr13:32972248-32973859	+	NM_000059	BRCA2
chr13:37677346-37679851	-	NM_145203	CSNK1A1L
chr13:40174918-40175577	-	NM_005780	LHFP
chr13:46733683-46733871	-	NM_002298	LCP1
chr13:49054083-49056076	+	NM_000321	RB1
chr13:52701451-52701690	-	NM_199289	NEK5
chr13:99173978-99174391	-	NM_003576	STK24
chr13:103527606-103528395	+	NM_000123	ERCC5
chr14:20784335-20784769	-	NM_182849	CCNB1IP1
chr14:24676271-24676765	+	NM_001184739	TSSK4
chr14:24808962-24809292	-	NM_006871	RIPK3
chr14:30396404-30396949	-	NM_002742	PRKD1
chr14:36989207-36989480	-	NM_001079668	NKX2-1
chr14:38678200-38682318	+	NM_001049	SSTR1
chr14:50862368-50862667	-	NM_004196	CDKL1
chr14:51223159-51225398	-	NM_020921	NIN
chr14:56147353-56147509	+	NM_182926	KTN1
chr14:62016352-62017748	+	NM_006255	PRKCH
chr14:67647470-67648575	+	NM_020806	GPHN
chr14:69061151-69062788	+	NM_133509	RAD51L1
chr14:71275432-71275938	-	NM_033141	MAP3K9
chr14:75387929-75388314	-	NM_031464	RPS6KL1
chr14:75593355-75593828	-	NM_033116	NEK9
chr14:78399512-78400347	+	NM_020421	ADCK1
chr14:81574842-81575344	+	NM_001142626	TSHR
chr14:91360706-91360977	-	NM_004755	RPS6KA5
chr14:92505840-92506453	-	NM_004239	TRIP11
chr14:93305660-93306354	+	NM_005113	GOLGA5
chr14:95557489-95557752	-	NM_177438	DICER1

chr14:96137617-96137874	+	NR_028288	TCL6
chr14:96178035-96178189	-	NM_021966	TCL1A
chr14:97347463-97348001	+	NM_003384	VRK1
chr14:99697631-99697944	-	NM_138576	BCL11B
chr14:102771248-102771581	-	NM_014226	RAGE
chr14:103523285-103523792	-	NM_006035	CDC42BPB
chr14:103934319-103934573	+	NM_002376	MARK3
chr14:105258884-105259109	-	NM_005163	AKT1
chr14:105258884-105259109	-	NM_005163	AKT1
chr15:34647638-34649981	+	NM_175741	C15orf55
chr15:40327177-40327847	+	NM_001013703	EIF2AK4
chr15:40509578-40509918	+	NM_001128628	PAK6
chr15:40512714-40513387	+	NM_001211	BUB1B
chr15:41803311-41803594	-	NM_002344	LTK
chr15:41870033-41871586	+	NM_006293	TYRO3
chr15:43170696-43170932	-	NM_173500	TTBK2
chr15:45803283-45803453	+	NR_022014	C15orf21
chr15:50978677-50979062	-	NM_017672	TRPM7
chr15:52356048-52358512	+	NM_002748	MAPK6
chr15:55710370-55710960	+	NM_001198784	FLJ27352
chr15:57511604-57511838	+	NM_207040	TCF12
chr15:64332318-64332516	-	NM_014326	DAPK2
chr15:64592467-64592972	-	NM_022048	CSNK1G1
chr15:66782789-66783932	+	NM_002755	MAP2K1
chr15:68098933-68099502	+	NM_145160	MAP2K5
chr15:74336511-74340205	+	NM_033238	PML
chr15:74921997-74922592	+	NM_003992	CLK3
chr15:75094621-75095589	+	NM_001127190	CSK
chr15:85411291-85416763	+	NM_020778	ALPK3
chr15:88524406-88524641	-	NM_001007156	NTRK3
chr15:90645457-90645758	-	NM_002168	IDH2
chr15:90645457-90645758	-	NM_002168	IDH2
chr15:91185116-91188627	+	NM_001042574	CRTC3
chr15:91358281-91358736	+	NM_000057	BLM
chr15:91434161-91434471	+	NM_001143783	FES
chr15:99500239-99507809	+	NM_000875	IGF1R
chr15:101608825-101610367	+	NM_024652	LRRK1
chr16:2132386-2132555	+	NM_000548	TSC2
chr16:2647601-2653239	+	NM_002613	PDPK1
chr16:3023088-3023304	-	NM_182687	PKMYT1
chr16:3841931-3842145	-	NM_004380	CREBBP
chr16:11017034-11017232	+	NM_000246	CIITA
chr16:11348223-11349435	-	NM_003745	SOCS1
chr16:11444448-11445667	+	NM_152308	C16orf75
chr16:12061376-12061975	+	NM_001192	TNFRSF17
chr16:12145653-12147191	+	NM_032167	RUNDCA
chr16:14041420-14046255	+	NM_005236	ERCC4

chr16:15931714-15932176	-	NM_001040113	MYH11
chr16:22295157-22300116	+	NM_013302	EEF2K
chr16:23652380-23652728	-	NM_024675	PALB2
chr16:23701130-23701738	+	NM_005030	PLK1
chr16:23724365-23724871	-	NM_033266	ERN2
chr16:27459804-27463413	+	NM_181078	IL21R
chr16:28331346-28335220	+	NM_001024401	SBK1
chr16:30002317-30003631	+	NM_004783	TAOK2
chr16:30128424-30128656	-	NM_001040056	MAPK3
chr16:30771389-30772547	+	NM_001172432	PHKG2
chr16:31123139-31124162	+	NM_001122957	BCKDK
chr16:31195131-31195373	+	NM_001170634	FUS
chr16:50810035-50810238	+	NM_015247	CYLD
chr16:56969262-56969437	+	NM_014685	HERPUD1
chr16:58231486-58231832	-	NM_001896	CSNK2A2
chr16:65038494-65038994	-	NM_001797	CDH11
chr16:67116065-67116292	+	NM_001755	CBFB
chr16:67961177-67963631	+	NM_006742	PSKH1
chr16:68867142-68869494	+	NM_004360	CDH1
chr16:68867142-68869494	+	NM_004360	CDH1
chr16:74725124-74725411	-	NM_152649	MLKL
chr16:79632631-79634672	-	NM_005360	MAF
chr16:89043014-89043554	-	NM_005187	CBFA2T3
chr16:89761288-89761510	+	NM_001098533	CDK10
chr16:89862263-89862476	-	NM_000135	FANCA
chr17:3627146-3630042	+	NM_031965	GSG2
chr17:3785500-3785714	-	NM_172207	CAMKK1
chr17:5076049-5078374	+	NM_004505	USP6
chr17:7579788-7579987	-	NM_001126112	TP53
chr17:7919710-7919922	+	NM_000180	GUCY2D
chr17:8053699-8054213	-	NM_002616	PER1
chr17:8113444-8113617	-	NM_004217	AURKB
chr17:9939700-9940114	-	NM_201432	GAS7
chr17:12044413-12047101	+	NM_003010	MAP2K4
chr17:17124434-17124992	-	NM_144606	FLCN
chr17:19286340-19286907	+	NM_139033	MAPK7
chr17:19679571-19679770	-	NM_001142610	ULK2
chr17:21217408-21218601	+	NM_145109	MAP2K3
chr17:27068926-27069834	+	NM_178170	NEK8
chr17:27869528-27871552	+	NM_020791	TAOK1
chr17:29579905-29580068	+	NM_001042492	NF1
chr17:30325626-30328107	+	NM_015355	SUZ12
chr17:34173859-34174287	+	NM_139215	TAF15
chr17:36881759-36886106	+	NM_005937	MLLT6
chr17:37074807-37078073	+	NM_006148	LASP1
chr17:37883891-37884965	+	NM_004448	ERBB2
chr17:37883891-37884965	+	NM_004448	ERBB2

chr17:38498220-38499169	+	NM_001024809	RARA
chr17:38498220-38499169	+	NM_001024809	RARA
chr17:40948653-40949134	+	NM_032387	WNK4
chr17:41258444-41258600	-	NR_027676	BRCA1
chr17:41622875-41623086	-	NM_001986	ETV4
chr17:48187270-48188473	+	NM_002611	PDK2
chr17:48278721-48279050	-	NM_000088	COL1A1
chr17:53397974-53402476	+	NM_002126	HLF
chr17:55709101-55710594	+	NM_170721	MSI2
chr17:56729176-56729413	-	NM_198393	TEX14
chr17:57771038-57774367	+	NM_004859	CLTC
chr17:58023861-58027836	+	NM_003161	RPS6KB1
chr17:59938757-59938980	-	NM_032043	BRIP1
chr17:60601546-60601742	+	NM_006852	TLK2
chr17:61712018-61712211	+	NM_203351	MAP3K3
chr17:62008644-62008798	-	NM_001039933	CD79B
chr17:62502143-62502534	-	NM_004396	DDX5
chr17:63553873-63554904	-	NM_004655	AXIN2
chr17:64799940-64806912	+	NM_002737	PRKCA
chr17:66526367-66528960	+	NM_002734	PRKAR1A
chr17:67537766-67538520	+	NM_002758	MAP2K6
chr17:74001328-74002130	+	NM_001258	CDK3
chr17:76993023-76993776	-	NM_001159772	CANT1
chr17:79975134-79975332	+	NM_024083	ASPSCR1
chr17:80203801-80203965	-	NM_139062	CSNK1D
chr18:672809-673549	+	NM_001071	TYMS
chr18:756506-756885	-	NM_005433	YES1
chr18:18690728-18691862	-	NM_005406	ROCK1
chr18:21061085-21063149	+	NM_003831	RIOK3
chr18:22930820-22930961	-	NM_015461	ZNF521
chr18:23670414-23670661	-	NM_001007559	SS18
chr18:48255477-48258246	+	NM_002747	MAPK4
chr18:56278870-56279099	-	NM_052947	ALPK2
chr18:56414586-56417420	+	NM_006785	MALT1
chr18:60985136-60986235	-	NM_000657	BCL2
chr18:60985136-60986235	-	NM_000657	BCL2
chr19:681599-683442	+	NM_005860	FSTL3
chr19:1615233-1615569	-	NM_003200	TCF3
chr19:1980097-1981386	+	NM_001319	CSNK1G2
chr19:2037419-2039905	-	NM_199054	MKNK2
chr19:3120936-3121504	+	NM_002067	GNA11
chr19:3785011-3785334	-	NM_139355	MATK
chr19:3969621-3969876	-	NM_001348	DAPK3
chr19:4123730-4124176	-	NM_030662	MAP2K2
chr19:4400270-4400521	-	NM_003025	SH3GL1
chr19:6270539-6270820	-	NM_005934	MLLT1
chr19:6590801-6591213	-	NM_001252	CD70

chr19:7150457-7150593	-	NM_000208	INSR
chr19:7977131-7979413	+	NM_145185	MAP2K7
chr19:10305445-10305805	-	NM_001379	DNMT1
chr19:10488839-10489152	-	NM_003331	TYK2
chr19:11151923-11152286	+	NM_001128845	SMARCA4
chr19:12984372-12985816	+	NM_014975	MAST1
chr19:13211600-13212059	-	NM_005583	LYL1
chr19:14228263-14228609	-	NM_002730	PRKACA
chr19:14551035-14551191	+	NM_213560	PKN1
chr19:15355470-15355623	-	NM_058243	BRD4
chr19:16187084-16187557	+	NM_003290	TPM4
chr19:17954992-17955289	-	NM_000215	JAK3
chr19:18632680-18632987	-	NM_006532	ELL
chr19:19624977-19626519	-	NM_032037	TSSK6
chr19:39108386-39108693	-	NM_007181	MAP4K1
chr19:39669013-39670096	+	NM_005884	PAK4
chr19:40317261-40317677	-	NM_004714	DYRK1B
chr19:40720826-40721532	+	NM_002446	MAP3K10
chr19:40771078-40771308	-	NM_001626	AKT2
chr19:40771078-40771308	-	NM_001626	AKT2
chr19:40895294-40896144	-	NM_144685	HIPK4
chr19:41220385-41220590	-	NM_024876	ADCK4
chr19:41745548-41745675	+	NM_021913	AXL
chr19:42383009-42383295	+	NM_021601	CD79A
chr19:42746284-42746786	-	NM_019884	GSK3A
chr19:42798925-42799999	+	NM_015125	CIC
chr19:45262634-45263351	+	NM_005178	BCL3
chr19:45303587-45303757	+	NM_012116	CBLC
chr19:45805581-45808591	+	NM_031417	MARK4
chr19:45873340-45873895	-	NM_001130867	ERCC2
chr19:45926477-45926870	-	NM_202001	ERCC1
chr19:46282985-46283911	-	NM_001081563	DMPK
chr19:47219337-47220434	-	NM_016457	PRKD2
chr19:50519230-50519470	-	NM_016440	VRK3
chr19:51380077-51380351	+	NM_001002231	KLK2
chr19:52729167-52729728	+	NM_014225	PPP2R1A
chr19:54079900-54083573	+	NM_018555	ZNF331
chr19:54409910-54410951	+	NM_002739	PRKCG
chr19:54618576-54619105	-	NM_013342	TFPT
chr19:55823228-55823953	+	NM_032430	BRSK1
chr19:57742377-57742724	+	NM_001015878	AURKC
chr19:59061693-59062132	+	NM_005762	TRIM28
chr2:11484071-11484761	-	NM_004850	ROCK2
chr2:12856947-12858753	+	NM_021643	TRIB2
chr2:16085564-16087179	+	NM_005378	MYCN
chr2:24991042-24993620	+	NM_147233	NCOA1
chr2:25475012-25475230	-	NM_153759	DNMT3A

chr2:27664524-27665174	+	NM_013392	NRBP1
chr2:30142808-30144482	-	NM_004304	ALK
chr2:30142808-30144482	-	NM_004304	ALK
chr2:37374780-37375015	-	NM_002759	EIF2AK2
chr2:37543329-37544272	-	NM_005813	PRKD3
chr2:39456455-39456723	-	NM_001009565	CDKL4
chr2:39663982-39664269	-	NM_003618	MAP4K3
chr2:42556823-42559738	+	NM_019063	EML4
chr2:46411823-46415179	+	NM_005400	PRKCE
chr2:47709867-47710410	+	NM_000251	MSH2
chr2:48033867-48034142	+	NM_000179	MSH6
chr2:58275965-58276152	+	NM_001130482	VRK2
chr2:60689366-60689609	-	NM_138559	BCL11A
chr2:61148847-61150228	+	NM_002908	REL
chr2:88926434-88927144	-	NM_004836	EIF2AK3
chr2:96930825-96931300	-	NM_017849	TMEM127
chr2:98350818-98351225	+	NM_207519	ZAP70
chr2:111435496-111435734	-	NM_004336	BUB1
chr2:112785877-112786995	+	NM_006343	MERTK
chr2:113286207-113290272	+	NM_153712	TTL
chr2:114035896-114036096	-	NM_003466	PAX8
chr2:128051579-128051802	-	NM_000122	ERCC3
chr2:135782145-135782298	-	NM_025052	YSK4
chr2:148684598-148688443	+	NM_001616	ACVR2A
chr2:158412554-158412894	-	NM_145259	ACVR1C
chr2:158655888-158656062	-	NM_001111067	ACVR1
chr2:169103687-169104155	-	NM_013233	STK39
chr2:171400351-171400550	+	NM_001171642	MYO3B
chr2:172016749-172017460	-	NM_012290	TLK1
chr2:173460506-173463912	+	NM_002610	PDK1
chr2:174130727-174132787	+	NM_016653	ZAK
chr2:176959157-176960716	+	NM_000523	HOXD13
chr2:176973584-176974366	+	NM_021192	HOXD11
chr2:178097069-178097340	-	NM_001145413	NFE2L2
chr2:179609996-179616816	-	NM_133379	TTN
chr2:190708639-190708856	+	NM_000534	PMS1
chr2:197027935-197028201	-	NM_004226	STK17B
chr2:201724352-201726239	-	NR_027856	CLK1
chr2:203424368-203432524	+	NM_001204	BMPR2
chr2:208425792-208425934	+	NM_134442	CREB1
chr2:209116103-209116341	-	NM_005896	IDH1
chr2:209116103-209116341	-	NM_005896	IDH1
chr2:213403122-213403402	-	NM_005235	ERBB4
chr2:213403122-213403402	-	NM_005235	ERBB4
chr2:216214208-216214546	+	NM_004044	ATIC
chr2:219566538-219567490	+	NM_015690	STK36
chr2:219849695-219850429	-	NM_017521	FEV

chr2:220113092-220115109	+	NR_026909	STK16
chr2:222436827-222437060	-	NM_004438	EPHA4
chr2:223158298-223159070	-	NM_000438	PAX3
chr2:223806164-223808169	+	NM_004457	ACSL3
chr2:234668868-234669847	+	NM_000463	UGT1A1
chr2:242082201-242082539	-	NM_015148	PASK
chr2:242447370-242447600	-	NM_006374	STK25
chr20:376791-378253	+	NM_021158	TRIB3
chr20:489044-489354	-	NM_001895	CSNK2A1
chr20:2097261-2098111	+	NM_080836	STK35
chr20:9624722-9625037	-	NM_020341	PAK7
chr20:30421469-30422550	+	NM_033118	MYLK2
chr20:30661471-30661671	+	NM_001172131	HCK
chr20:31022184-31027172	+	NM_015338	ASXL1
chr20:36031523-36033871	+	NM_198291	SRC
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chr20:39314466-39317926	-	NM_005461	MAFB
chr20:39751784-39753176	+	NM_003286	TOP1
chr20:42195062-42195221	+	NM_170693	SGK2
chr20:43280165-43280426	-	NM_000022	ADA
chr20:43703608-43708643	+	NM_006282	STK4
chr20:45317720-45318326	-	NM_033550	TP53RK
chr20:54963161-54963308	-	NM_003600	AURKA
chr20:57414744-57415991	+	NM_016592	GNAS
chr20:60754187-60757616	+	NM_198935	SS18L1
chr20:62168387-62168757	-	NM_005975	PTK6
chr20:62178410-62178907	-	NM_080823	SRMS
chr21:33370788-33376427	+	NM_014586	HUNK
chr21:34399058-34401550	+	NM_005806	OLIG2
chr21:34911426-34911679	-	NM_001136005	GART
chr21:36259089-36261037	-	NM_001001890	RUNX1
chr21:38878351-38878707	+	NM_101395	DYRK1A
chr21:39947535-39947721	-	NM_004449	ERG
chr21:42869995-42870166	-	NM_005656	TMPRSS2
chr21:43186969-43187299	-	NM_020639	RIPK4
chr22:19118270-19120186	+	NM_053006	TSSK2
chr22:22123433-22123659	-	NM_002745	MAPK1
chr22:23657569-23660274	+	NM_004327	BCR
chr22:24133892-24134131	+	NM_003073	SMARCB1
chr22:26118205-26125308	+	NM_005160	ADRBK2
chr22:28192700-28197536	-	NM_002430	MN1
chr22:29130340-29130765	-	NM_007194	CHEK2
chr22:29687500-29687638	+	NM_001163286	EWSR1
chr22:30078958-30079954	+	NM_181825	NF2
chr22:31672724-31673674	+	NM_001031801	LIMK2
chr22:36744898-36745350	-	NM_002473	MYH9
chr22:38710036-38710224	-	NM_152221	CSNK1E

chr22:39636809-39636964	-	NM_033016	PDGFB
chr22:40859174-40859340	-	NM_020831	MKL1
chr22:41572726-41576131	+	NM_001429	EP300
chr22:42526563-42526933	-	NM_000106	CYP2D6
chr22:50356537-50357770	+	NM_001001852	PIM3
chr22:50699763-50700139	-	NM_002969	MAPK12
chr22:50708555-50708829	-	NM_002751	MAPK11
chr3:9074283-9074486	-	NM_014850	SRGAP3
chr3:9809300-9809515	-	NM_003656	CAMK1
chr3:10142821-10143664	+	NM_001018115	FANCD2
chr3:10191420-10193796	+	NM_000551	VHL
chr3:10283749-10285477	+	NM_001570	IRAK2
chr3:12392950-12393223	+	NM_015869	PPARG
chr3:12659963-12660296	-	NM_002880	RAF1
chr3:12659963-12660296	-	NM_002880	RAF1
chr3:27326280-27326502	-	NM_199347	NEK10
chr3:30732861-30735683	+	NM_001024847	TGFBR2
chr3:37038064-37038250	+	NM_001167618	MLH1
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chr3:38181828-38182133	+	NM_001172567	MYD88
chr3:38294257-38297029	+	NM_005109	OXSR1
chr3:38524578-38534683	+	NM_001106	ACVR2B
chr3:41280574-41281989	+	NM_001904	CTNNB1
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chr3:41996063-41996349	-	NM_017886	ULK4
chr3:43388780-43392684	+	NM_001100594	SNRK
chr3:47161621-47166088	-	NM_014159	SETD2
chr3:49899676-49899885	-	NM_024046	CAMKV
chr3:49939762-49941356	-	NM_002447	MST1R
chr3:50685274-50686769	+	NM_004635	MAPKAPK3
chr3:52443807-52444059	-	NM_004656	BAP1
chr3:52621318-52621501	-	NM_018313	PBRM1
chr3:52802303-52802670	-	NM_003157	NEK4
chr3:53226073-53226783	+	NM_006254	PRKCD
chr3:58410428-58410928	+	NM_017771	PXK
chr3:60522542-60522762	-	NM_001166243	FHIT
chr3:69987452-69988266	+	NM_001184968	MITF
chr3:71246983-71247269	-	NM_001012505	FOXP1
chr3:89528496-89531334	+	NM_005233	EPHA3
chr3:100455369-100455598	+	NM_001195479	TFG
chr3:105586203-105586485	-	NM_170662	CBLB
chr3:119812143-119813314	-	NM_002093	GSK3B
chr3:123451692-123451999	-	NM_053025	MYLK
chr3:124281639-124281986	+	NM_001024660	KALRN
chr3:128200611-128200795	-	NM_001145662	GATA2
chr3:128369332-128369769	-	NM_002950	RPN1
chr3:130463279-130464158	-	NM_014602	PIK3R4

chr3:130992271-130992468	+	NM_024800	NEK11
chr3:138663015-138666032	-	NM_023067	FOXL2
chr3:141535505-141535942	+	NM_139209	GRK7
chr3:142297437-142297718	-	NM_001184	ATR
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chr3:170020777-170023820	+	NM_002740	PRKCI
chr3:178951831-178952547	+	NM_006218	PIK3CA
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chr3:184299251-184300246	+	NM_004443	EPHB3
chr3:185200092-185200678	+	NM_004721	MAP3K13
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chr3:186506863-186507735	+	NM_001967	EIF4A2
chr3:187451270-187451541	-	NM_001706	BCL6
chr3:188326898-188327682	+	NM_005578	LPP
chr3:195622066-195622482	-	NM_001010938	TNK2
chr3:195803884-195804043	-	NM_001128148	TFRC
chr3:196555139-196559568	+	NM_002577	PAK2
chr4:925780-926224	-	NM_005255	GAK
chr4:1805368-1805613	+	NM_000142	FGFR3
chr4:1805368-1805613	+	NM_000142	FGFR3
chr4:1944015-1950595	+	NM_133334	WHSC1
chr4:2986189-2986385	+	NM_182982	GRK4
chr4:5500621-5502775	+	NM_018401	STK32B
chr4:41750336-41751037	-	NM_003924	PHOX2B
chr4:48136121-48136323	-	NM_003328	TXK
chr4:48230443-48230726	-	NM_003215	TEC
chr4:54245189-54245334	+	NM_030917	FIP1L1
chr4:54930298-54930838	-	NM_012110	CHIC2
chr4:55161241-55164462	+	NM_006206	PDGFRA
chr4:55591972-55592254	+	NM_001093772	KIT
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chr4:55991343-55991812	-	NM_002253	KDR
chr4:66535229-66535703	-	NM_004439	EPHA5
chr4:71895018-71896679	+	NM_000788	DCK
chr4:76550954-76551251	-	NM_003948	CDKL2
chr4:79799837-79800644	+	NM_017593	BMP2K
chr4:82125690-82126265	-	NM_006259	PRKG2
chr4:87028325-87028856	-	NM_138981	MAPK10
chr4:96075648-96079651	+	NM_001203	BMPR1B
chr4:99342358-99342595	+	NM_021159	RAP1GDS1
chr4:103454954-103455092	+	NM_001165412	NFKB1
chr4:106155003-106163978	+	NM_017628	TET2
chr4:113298783-113299104	+	NM_025144	ALPK1
chr4:114378396-114378769	-	NM_172127	CAMK2D
chr4:123377398-123377700	-	NM_000586	IL2
chr4:128804366-128804562	+	NM_001190801	PLK4
chr4:153303290-153303714	-	NM_001013415	FBXW7

chr5:14507938-14509508	+	NM_007118	TRIO
chr5:38530557-38530818	-	NM_001127671	LIFR
chr5:40774979-40775124	-	NM_206907	PRKAA1
chr5:43280031-43281002	+	NM_153361	MGC42105
chr5:55271992-55272171	-	NM_002184	IL6ST
chr5:56189307-56192028	+	NM_005921	MAP3K1
chr5:57755466-57755963	-	NM_006622	PLK2
chr5:67576704-67576884	+	NM_181523	PIK3R1
chr5:68572883-68573307	+	NM_001799	CDK7
chr5:96502399-96503745	-	NM_001159749	RIOK2
chr5:108523083-108523423	+	NM_005246	FER
chr5:110819673-110820798	+	NM_001744	CAMK4
chr5:112173199-112181986	+	NM_000038	APC
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chr5:122940982-122941106	+	NM_001044723	CSNK1G3
chr5:147211035-147211310	-	NM_003122	SPINK1
chr5:149465891-149466220	-	NM_005211	CSF1R
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chr5:149669076-149669453	-	NM_015981	CAMK2A
chr5:149792137-149792373	-	NM_001025159	CD74
chr5:151055642-151055812	-	NM_003118	SPARC
chr5:156679566-156682159	+	NM_005546	ITK
chr5:158526302-158526838	-	NM_024007	EBF1
chr5:170725715-170727069	+	NM_022897	RANBP17
chr5:170738342-170739188	+	NM_021025	TLX3
chr5:170833350-170833781	+	NM_001037738	NPM1
chr5:171614840-171615396	-	NM_005990	STK10
chr5:176520282-176520602	+	NM_022963	FGFR4
chr5:176520282-176520602	+	NM_022963	FGFR4
chr5:176562891-176563081	+	NM_172349	NSD1
chr5:176868687-176869900	+	NM_001004106	GRK6
chr5:178050206-178050467	-	NM_020666	CLK4
chr5:179674804-179674976	-	NM_139069	MAPK9
chr5:180028455-180030440	-	NM_182925	FLT4
chr6:397057-397302	+	NM_002460	IRF4
chr6:3113236-3115471	+	NM_003804	RIPK1
chr6:4060596-4065267	+	NM_003913	PRPF4B
chr6:7402829-7403180	+	NM_153005	RIOK1
chr6:10830730-10831160	-	NM_005906	MAK
chr6:18149168-18149452	-	NM_000367	TPMT
chr6:18264023-18264277	-	NM_003472	DEK
chr6:27107037-27107507	+	NM_003495	HIST1H4I
chr6:28890939-28891818	-	NM_006510	TRIM27
chr6:30865105-30865424	+	NM_001954	DDR1
chr6:31137942-31138501	-	NM_002701	POU5F1
chr6:31544842-31546162	+	NM_000594	TNF

chr6:31946629-31946837	+	NM_032454	STK19
chr6:32948308-32949332	+	NM_005104	BRD2
chr6:33167968-33168482	-	NM_021976	RXRB
chr6:33289445-33289735	-	NM_001141970	DAXX
chr6:34208463-34208709	+	NM_145903	HMGA1
chr6:35433970-35434931	+	NM_021922	FANCE
chr6:36070297-36070476	+	NM_001315	MAPK14
chr6:36107020-36107892	+	NM_002754	MAPK13
chr6:36507798-36508034	-	NM_007271	STK38
chr6:37141659-37143254	+	NM_002648	PIM1
chr6:41658688-41659023	-	NM_007162	TFEB
chr6:41909139-41909602	-	NM_001136125	CCND3
chr6:43109618-43109829	+	NM_152882	PTK7
chr6:43252670-43256047	+	NM_032538	TTBK1
chr6:52905883-52906256	-	NM_016513	ICK
chr6:80736047-80736281	+	NM_001166691	TTK
chr6:91296432-91296957	-	NM_145332	MAP3K7
chr6:94128912-94129350	-	NM_004440	EPHA7
chr6:106554735-106557864	+	NM_001198	PRDM1
chr6:112020667-112020923	-	NM_153047	FYN
chr6:116381080-116381971	-	NM_002031	FRK
chr6:117746646-117747068	-	NM_002944	ROS1
chr6:117923116-117923755	-	NM_020399	GOPC
chr6:135516835-135517142	+	NM_001161658	MYB
chr6:137112797-137113706	-	NM_005923	MAP3K5
chr6:138202121-138204499	+	NM_006290	TNFAIP3
chr6:150022864-150023452	-	NM_004690	LATS1
chr6:152128763-152129549	+	NM_000125	ESR1
chr6:161519259-161519509	+	NM_005922	MAP3K4
chr6:167275545-167275821	-	NM_001006932	RPS6KA2
chr6:167426945-167427105	+	NM_007045	FGFR1OP
chr6:168351815-168352917	+	NM_001040000	MLLT4
chr7:2998083-2998315	-	NM_032415	CARD11
chr7:6045472-6045707	-	NR_003085	PMS2
chr7:6082513-6082671	-	NM_001134335	EIF2AK1
chr7:23751675-23751814	+	NM_001122833	STK31
chr7:26240141-26240463	-	NM_031243	HNRNPA2B1
chr7:27204446-27205199	-	NM_152739	HOXA9
chr7:27224004-27224885	-	NM_005523	HOXA11
chr7:27238724-27239775	-	NM_000522	HOXA13
chr7:28220031-28220487	-	NM_175061	JAZF1
chr7:43664066-43667028	+	NM_004760	STK17A
chr7:44268936-44269150	-	NM_001220	CAMK2B
chr7:55272898-55275081	+	NM_005228	EGFR
chr7:55272898-55275081	+	NM_005228	EGFR
chr7:56156501-56156718	-	NM_006213	PHKG1
chr7:66460226-66460638	-	NM_016038	SBDS

chr7:73457382-73457548	+	NM_001081753	ELN
chr7:73535418-73536904	+	NM_002314	LIMK1
chr7:75368068-75368329	-	NM_005338	HIP1
chr7:91699293-91699570	+	NM_005751	AKAP9
chr7:92462354-92463054	-	NM_001259	CDK6
chr7:95225425-95225975	-	NM_002612	PDK4
chr7:97834725-97838994	+	NM_014916	LMTK2
chr7:98609643-98610914	+	NM_003496	TRRAP
chr7:100424550-100425193	-	NM_004444	EPHB4
chr7:104909202-104909527	-	NM_182691	SRPK2
chr7:116399394-116399594	+	NM_000245	MET
chr7:116399394-116399594	+	NM_000245	MET
chr7:128851814-128853435	+	NM_005631	SMO
chr7:137686299-137686896	-	NM_194071	CREB3L2
chr7:138239392-138239659	+	NM_003852	TRIM24
chr7:140394412-140394958	+	NM_052853	ADCK2
chr7:140624315-140624614	-	NM_004333	BRAF
chr7:140624315-140624614	-	NM_004333	BRAF
chr7:141426953-141427228	-	NR_015392	FLJ40852
chr7:142568498-142568897	+	NM_004445	EPHB6
chr7:143105766-143106035	-	NM_005232	EPHA1
chr7:148529675-148529892	-	NM_004456	EZH2
chr7:148529675-148529892	-	NM_004456	EZH2
chr7:150776536-150777059	-	NM_006712	FASTK
chr7:152132660-152133140	-	NM_170606	MLL3
chr8:11421361-11422158	+	NM_001715	BLK
chr8:27315760-27316953	+	NM_004103	PTK2B
chr8:27690522-27690700	-	NM_018492	PBK
chr8:31030460-31031327	+	NM_000553	WRN
chr8:38173884-38175606	-	NM_017778	WHSC1L1
chr8:38277006-38277303	-	NM_001174064	FGFR1
chr8:38277006-38277303	-	NM_001174064	FGFR1
chr8:42174177-42174779	+	NM_001190722	IKBKB
chr8:42229030-42229363	+	NM_002690	POLB
chr8:42873450-42885732	+	NM_032410	HOOK3
chr8:56854363-56854600	+	NM_002350	LYN
chr8:57025450-57026591	-	NM_005372	MOS
chr8:57080536-57080995	-	NM_001114634	PLAG1
chr8:57125270-57125518	+	NM_001011668	CHCHD7
chr8:67771595-67774307	+	NM_001033578	SGK3
chr8:87081614-87081901	-	NM_033126	PSKH2
chr8:90802256-90803342	+	NM_003821	RIPK2
chr8:100904085-100904330	-	NM_004374	COX6C
chr8:119122273-119124108	-	NM_000127	EXT1
chr8:126448197-126450694	+	NM_025195	TRIB1
chr8:128752591-128753730	+	NM_002467	MYC
chr8:141900591-141900918	-	NM_005607	PTK2

chr8:144804194-144804683	+	NM_139021	MAPK15
chr8:144921004-144921160	-	NM_178564	NRBP2
chr8:145618133-145618503	+	NM_174922	ADCK5
chr9:5126633-5128233	+	NM_004972	JAK2
chr9:5467789-5470617	+	NM_014143	CD274
chr9:14313430-14314095	-	NM_001190737	NFIB
chr9:20622193-20622564	-	NM_004529	MLLT3
chr9:21994087-21994540	-	NM_058195	CDKN2A
chr9:21994087-21994540	-	NM_058195	CDKN2A
chr9:27229105-27230222	+	NM_000459	TEK
chr9:32629401-32635717	-	NM_153809	TAF1L
chr9:35079387-35080063	-	NM_004629	FANCG
chr9:35608808-35610088	+	NM_006285	TESK1
chr9:35809326-35809778	+	NM_003995	NPR2
chr9:36677106-36677729	+	NM_014791	MELK
chr9:37033932-37034526	-	NM_016734	PAX5
chr9:71627398-71629089	-	NM_002732	PRKACG
chr9:77502689-77503060	-	NM_017662	TRPM6
chr9:80645965-80646269	-	NM_002072	GNAQ
chr9:87425406-87430671	+	NM_001007097	NTRK2
chr9:90320996-90323599	+	NM_004938	DAPK1
chr9:93629362-93629531	+	NM_003177	SYK
chr9:94712098-94712494	-	NM_004560	ROR2
chr9:95178850-95179906	-	NM_005014	OMD
chr9:98011358-98011701	-	NM_000136	FANCC
chr9:100459352-100459741	-	NR_027302	XPA
chr9:101911411-101916523	+	NM_004612	TGFBR1
chr9:102595513-102596391	+	NM_173199	NR4A3
chr9:108424687-108425435	+	NM_005421	TAL2
chr9:127113065-127114769	+	NM_001166170	NEK6
chr9:130551406-130553102	+	NM_001261	CDK9
chr9:131451458-131451984	+	NM_003011	SET
chr9:131482622-131483249	+	NM_013355	PKN3
chr9:133759305-133763108	+	NM_005157	ABL1
chr9:134108790-134109141	+	NM_005085	NUP214
chr9:135785907-135786126	-	NM_001162426	TSC1
chr9:135996308-135996611	-	NM_006266	RALGDS
chr9:136270325-136271270	+	NM_153710	C9orf96
chr9:136918336-136918762	-	NM_007371	BRD3
chr9:139440127-139440288	-	NM_017617	NOTCH1
chrX:1581415-1585525	-	NM_178129	P2RY8
chrX:3631078-3631725	-	NM_005044	PRKX
chrX:15574145-15574702	+	NM_001721	BMX
chrX:18671501-18671799	+	NM_001037343	CDKL5
chrX:19431424-19431632	-	NM_001001671	MAP3K15
chrX:20284631-20284800	-	NM_004586	RPS6KA3
chrX:24551995-24552592	+	NM_005391	PDK3

chrX:41394095-41394276	-	NM_001126055	CASK
chrX:44970576-44971895	+	NM_021140	KDM6A
chrX:47430671-47431370	+	NM_001654	ARAF
chrX:48125671-48125876	+	NM_005635	SSX1
chrX:48252147-48252835	+	NM_005636	SSX4
chrX:48549447-48549867	+	NM_000377	WAS
chrX:48652149-48652767	+	NM_002049	GATA1
chrX:48776000-48776463	-	NM_006875	PIM2
chrX:48900586-48901040	-	NM_006521	TFE3
chrX:52734680-52734869	-	NM_175698	SSX2
chrX:53249970-53250148	-	NM_004187	KDM5C
chrX:54265250-54265582	-	NM_020922	WNK3
chrX:64959540-64961843	+	NM_002444	MSN
chrX:66763823-66766654	+	NM_000044	AR
chrX:70519741-70521068	+	NM_007363	NONO
chrX:70596812-70597091	+	NM_138923	TAF1
chrX:77041417-77041769	-	NM_000489	ATRX
chrX:83442776-83442993	-	NM_014496	RPS6KA6
chrX:100630081-100630352	-	NM_000061	BTK
chrX:108718385-108719300	-	NM_001522	GUCY2F
chrX:110463535-110464223	+	NM_001128166	PAK3
chrX:118749637-118750755	-	NM_145800	SEPT6
chrX:129215179-129215563	-	NM_001127197	ELF4
chrX:133087074-133087288	-	NM_001164618	GPC3
chrX:152938413-152938583	-	NM_001039582	PNCK
chrX:153049525-153049718	+	NM_001170761	SRPK3
chrX:153279442-153279779	-	NM_001025242	IRAK1
chrX:154294130-154294382	-	NM_001018025	MTCP1
chrY:7235346-7235524	+	NR_028062	PRKY

**Supplementary Table 4: Patient information**

Patient ID	Enrollment	Collection date	Gender	Age	Cancer Tissue of Origin	Cancer subtype
Patient 3	5/2/11	5/9/11	M	46	Colorectal	Adenocarcinoma
Patient 4	5/3/11	5/9/11	F	48	Melanoma	Ulcerated Spitzoid

**Supplementary Table 5: Alignment statistics**

Patient	Sample	Paired-end Reads	Read Length	GC %	Mapped PE Reads	Estimated Coverage*	Exome Capture Kit
Patient 1	Genome	78371278	101	40	57970138	3.76X	NA
Patient 1	Tumor Exome	80242182	101	46	60755700	86X	Agilent v38
Patient 1	Normal Exome	85973358	101	47	69262590	101X	Agilent v38
Patient 1	Transcriptome	71251099	101	48	42456155	NA	NA
Patient 2	Genome	78995841	101	41	65743483	4.27X	NA
Patient 2	Tumor Exome	79504696	101	47	62494687	82X	Agilent v38
Patient 2	Normal Exome	83348497	101	48	67025566	87X	Agilent v38
Patient 2	Transcriptome	88651687	101	49	54829733	NA	NA
Patient 3	Genome	88984288	101	44	73971052	4.8X	NA
Patient 3	Tumor Exome	92874149	101	44	81713096	126X	Roche V2.0
Patient 3	Normal Exome	93344376	101	45	81116604	128X	Roche V2.0
Patient 3	Transcriptome	94531888	101	47	52971002	NA	NA
Patient 4	Genome	84867888	101	42	74140062	4.8X	NA
Patient 4	Tumor Exome	92302441	101	44	81037501	124X	Roche V2.0
Patient 4	Normal Exome	91403534	101	46	79102039	121X	Roche V2.0
Patient 4	Transcriptome	118581455	101	48	88866978	NA	NA

- For exome capture data, the Bowtie/in-house pipeline results were used in this table

Table S6: SNVs Patient 1

Gene	Aberration		BWA/GATK Pipeline			Bowtie/In House Pipeline		
	Nucleotide change	Amino acid change	Position (hg19)	Variant Reads	Total Reads	Position (hg18)	Variant Reads	Total Reads
'ABCA12(NM_015657)&ABCA12(NM_173076)'	G>T	'Ala1736Glu[-]&Ala2054Glu[+]'>T	chr2@215821459	76	204	chr2:215529704	47	112
'ADCY4(NM_001198568)'	G>C	'Ala752Gly[-]'>C	chr14@24792197	9	28			
'ADK(NM_006721)[+]&ADK(NM_001123)[+]'>T	A>T	'None&None'	chr10@76349033	22	87			
'ANKRD20A4(NM_001098805)'	A>C	'Thr667Pro[+]'>C	chr9@69423703	15	59			
'AP4S1(NM_001128126)'	G>T	'Ala133Ser[+]'>T	chr14@31562203	18	66			
'ARC(NM_015193)'	A>C	'Val231Gly[-]'>C	chr8@143694941	21	35			
'ATXN2L(NM_007245)'	G>T	'Glu1075Asp[+]'>T	chr16@28847583	24	89			
'BAI3(NM_001704)'	C>T	'Arg982Cys[+]'>T	chr6@70034893	29	108	chr6:70091614	19	69
'BCL9(NM_004326)'	A>G	'Asn1101Ser[+]'>G	chr1@147095781	94	448			
'BID(NM_001196)&BID(NM_197966)'	C>G	'Ser64Thr[-]&Ser110Thr[-]'>G	chr22@18226601	39	47			
'BRD8(NM_006696)'	C>T	'Val249Ile[-]'>T	chr5@137504275	21	92			
'BTBD7(NM_001002860)'	G>T	'Thr326Lys[-]'>T	chr14@93760389	32	93			
'BTBD7(NM_001002860)'	C>T	'Val280Ile[-]'>T	chr14@93760528	29	88			
'BTBD7(NM_001002860)'	A>G	'Ser232Pro[-]'>G	chr14@93760672	25	84			
'C1R(NM_001733)'	G>A	'Arg-506stop[-]'>A	chr12@7242710	10	46			
'CACNA1B(NM_000718)[+]'>G	C>G	'None'	chr9@140773503	10	33			
'CDC42BPA(NM_014826)[-]&CDC42BPA(NM_00360)'	A>G	'None&None'	chr1@227330644	19	66			
'CDC45(NM_001178010)&CDC45(NM_001178011)'	G>A	'Ala129Thr[+]&Ala83Thr[+]'>A	chr22@19471427	34	95	chr22:17851427	27	64
'CELF5(NM_001172673)'	G>C	'Ala379Pro[+]'>C	chr19@3290293	17	83			
'CNTN6(NM_014461)[+]'>T	T>G	'None'	chr3@1443994	39	77			
'CPM(NM_001874)'	G>A	'Pro404Ser[-]'>A	chr12@69250339	22	85	chr12:67536606	15	64
'CTAGE6P(NM_178561)'	T>A	'Thr348Ser[-]'>A	chr7@143453710	38	112			
'CYP21A2(NM_000500)'	A>T	'His63Leu[+]'>T	chr6@31973653	18	55			
'DIAPH3(NM_001042517)&DIAPH3(NM_030932)'	T>C	'Asn863Asp[-]&Asn600Asp[+]'>C	chr13@60453383	39	154			
'DNAH17(NM_173628)'	G>A	'Arg3232Cys[-]'>A	chr17@76455250	103	181			
'DUX4L6(NM_001127388)'	G>C	'Gly214Ala[+]'>C	chr10@135491030	51	170			
'DYRK1A(NM_130436)&DYRK1A(NM_001396)'	A>G	'Thr729Ala[+]&Thr738Ala[+]'>G	chr21@38884754	39	150			
'EWSR1(NM_001163285)&EWSR1(NM_001163286)'	A>T	'Met294Leu[+]&Met238Leu[+]'>T	chr22@29684681	19	55			
'EXT1(NM_000127)'	G>C	'His48Gln[-]'>C	chr8@119123142	19	95			
'FAM22G(NM_001170741)'	G>A	'Gly502Asp[+]'>A	chr9@99700710	36	104			
'FBXW2(NM_012164)'	C>A	'Ala116Ser[-]'>G	chr9@123550191	44	204			
'FCGBP(NM_003890)'	G>C	'Gln4124Glu[-]'>T	chr19@40370296	22	70			
'FOXP1(NM_005249)'	G>C	'Glu173Asp[+]'>T	chr14@29237004	11	37			
'FOXP1(NM_005249)'	G>C	'Ser430Thr[+]'>T	chr14@29237774	24	105			

'FXYD2(NM_001680)&FXYD2(NM_021603)'	C>T	'Arg51His[-]&Arg49His[-]'	chr11@117691598	57	117	chr11:117196808	41	80
GLT25D2	C>T	Val232Ile				chr1:182205164	15	108
'GPR98(NM_032119)'	A>G	'Lys2253Arg[+]'	chr5@89986665	51	208			
'HECTD1(NM_015382)'	C>G	'Gly1400Ala[-]'	chr14@31598378	73	296			
'HNRNPR(NM_001102399)&HNRNPR(NM_005826)'	A>C	'Ser463Ala[-]&Ser561Ala[-]'	chr1@23637168	77	292			
'HOXC4(NM_014620)'	G>C	'Gly80Ala[+]'	chr12@54447945	24	80			
'HOXC5(NM_018953)'	C>T	'Pro86Leu[+]'	chr12@54427163	9	39			
'HUWE1(NM_031407)'	C>A	'Val1888Leu[-]'	chrX@53607845	72	72	chrX:53624570	54	54
'JPH1(NM_020647)'	C>A	'Gly51Val[-]'	chr8@75233371	22	67			
KCND2	C>G	Asp151Glu				chr7:119702375	9	79
'KDM5C(NM_001146702)&KDM5C(NM_004187)'	A>C	'Val858Gly[-]&Val925Gly[-]'	chrX@53226075	16	27			
'KIAA1486(NM_020864)'	C>T	'Arg48Cys[+]'	chr2@226273738	207	351			
'KIR2DS4(NM_012314)'	T>C	'Ile123Thr[+]'	chr19@55349328	122	122			
'KIR2DS4(NM_012314)'	G>T	'Leu111Phe[+]'	chr19@55349293	34	90			
'LIMK1(NM_002314)'	A>C	'His614Pro[+]'	chr7@73535528	39	53			
'LIN54(NM_194282)'	A>G	'Ser173Pro[-]'	chr4@83905481	57	180			
'LIN54(NM_194282)'	T>C	'Thr169Ala[-]'	chr4@83905493	56	201			
'LIN54(NM_194282)'	T>A	'Thr83Ser[-]'	chr4@83905751	53	192			
'LIN54(NM_194282)'	T>C	'Ile82Val[-]'	chr4@83905754	52	190			
'LRP6(NM_002336)'	G>C	'Thr83Ser[-]'	chr12@12397397	25	114			
'LRRC8A(NM_019594)'	C>T	'Ala591Val[+]'	chr9@131671215	32	153			
'MAF(NM_001031804)'	C>T	'Ser8Asn[-]'	chr16@79633777	11	21			
'MAOB(NM_000898)'	C>G	'Arg415Pro[-]'	chrX@43628657	36	102			
'MAP1B(NM_005909)'	G>A	'Arg558His[+]'	chr5@71490855	50	164	chr5:71526611	33	105
'MATR3(NM_001194954)'	G>A	'Ala105Thr[+]'	chr5@138643417	91	232			
'MBNL1(NM_207296)[+]'	G>A	'None'	chr3@152175914	17	82			
'MBNL2(NM_144778)'	G>A	'Ser211Asn[+]'	chr13@97999149	10	41			
'MGA(NM_001164273)'	G>C	'Ser1472Thr[+]'	chr15@42028877	31	110			
'MSL1(NM_001012241)'	G>A	'Ser74Asn[+]'	chr17@38285515	29	116			
'MSL2(NM_001145417)&MSL2(NM_018133)'	T>A	'Thr349Ser[-]&Thr423Ser[-]'	chr3@135870456	45	174			
'MUC4(NM_018406)'	G>C	'Thr4100Ser[-]'	chr3@195506152	52	152			
'MUC4(NM_018406)'	G>T	'Pro2514His[-]'	chr3@195510910	205	960			
'MYST4(NM_012330)'	T>C	'Ile413Thr[+]'	chr10@76735333	33	141			
'MYST4(NM_012330)'	A>T	'Thr416Ser[+]'	chr10@76735341	33	140			
'NDST4(NM_022569)'	G>A	'Arg679stop[-]'	chr4@115767059	82	118	chr4:115986508	47	60
'NFIB(NM_001190737)'	C>T	'Gly418Ser[-]'	chr9@14116339	48	240			
'OR11H12(NM_001013354)'	T>A	'Leu146His[+]'	chr14@19378030	116	505			
'OSBPL11(NM_022776)'	T>A	'Leu487Phe[-]'	chr3@125271218	34	34			

'OTUD7B(NM_020205)'	A>T	'Asn144Lys[-]'	chr1@149939289	24	119			
'PAPPA(NM_002581)[+]'	C>T	'None'	chr9@119097132	18	83			
'PCDH7(NM_001173523)[+]&PCDH7(NM_032457)[-]	G>A	'None&None'	chr4@30921771	38	111			
'PCDHB7(NM_018940)'	G>A	'Ala28Thr[+]'	chr5@140552498	113	204	chr5:140532682	66	124
'PCNT(NM_006031)'	C>T	'Thr328Ile[+]'	chr21@47864612	49	66	chr21:46689040	25	34
PEA15	G>C	Lys99Asn				chr1:158449615	21	87
'PHF3(NM_015153)'	G>A	'Ala36Thr[+]'	chr6@64356562	54	171			
'PKD1(NM_000296)'	C>G	'Ala3053Pro[-]'	chr16@2152426	18	63			
'PKD1L2(NM_052892)'	A>G	'Leu-105Pro[-]'	chr16@81142821	61	61			
'PKHD1(NM_138694)[-]&PKHD1(NM_170724)[-]'	G>A	'None&None'	chr6@51875265	30	139			
'PPP2R5A(NM_006243)'	G>T	'Ser93Ile[+]'	chr1@212502573	45	116			
PRDM2	G>C	Gly932Ala, 731				chr1:13979672	18	129
'PROX1(NM_002763)'	A>G	'Met154Val[+]'	chr1@214170338	64	309			
'PTEN(NM_000314)[+]'	T>C	'None'	chr10@89693014	18	18			
'PTEN(NM_000314)[+]'	A>G	'None'	chr10@89693016	16	16			
'PYHIN1(NM_198930)&PYHIN1(NM_198929)'	C>A	'Thr236Lys[+]&Thr245Lys[+]	chr1@158911921	25	86			
'RBM12B(NM_203390)'	G>T	'Thr24Lys[-]'	chr8@94748568	59	234			
'RBM14(NM_006328)'	G>A	'Val159Ile[+]'	chr11@66391822	26	103			
'RBM14(NM_006328)'	G>C	'Gly156Ala[+]'	chr11@66391814	24	100			
'RECQL(NM_002907)[-]&RECQL(NM_032941)[-]'	C>A	'None&None'	chr12@21623281	15	61			
'RIMS2(NM_001100117)[+]&RIMS2(NM_014677)[+]	G>A	'None&None'	chr8@105025663	37	142			
'SELL(NM_000655)'	C>G	'Ala159Pro[-]'	chr1@169677594	77	265			
SLC10A5	G>C	Ala19Gly				chr8:82769707	9	59
SLTRK1	C>T	Arg646Gln				chr13:83351707	6	47
'SLTM(NM_001013843)&SLTM(NM_024755)'	G>T	'His214Asn[-]&His232Asn[-]	chr15@59192032	55	189			
'SLTM(NM_001013843)&SLTM(NM_024755)'	T>C	'Thr215Ala[-]&Thr233Ala[-]	chr15@59192029	57	200			
'SLTM(NM_001013843)&SLTM(NM_024755)'	G>C	'Asp297Glu[-]&Asp315Glu[-]	chr15@59191781	50	189			
'SLTM(NM_001013843)&SLTM(NM_024755)'	C>A	'Gly264Val[-]&Gly282Val[-]'	chr15@59191881	49	186			
'SLTM(NM_001013843)&SLTM(NM_024755)'	A>C	'Val217Gly[-]&Val235Gly[-]'	chr15@59192022	56	214			
'SLTM(NM_001013843)&SLTM(NM_024755)'	A>C	'Ser307Ala[-]&Ser325Ala[-]'	chr15@59191753	54	211			
'SLTM(NM_001013843)&SLTM(NM_024755)'	C>G	'Cys293Ser[-]&Cys311Ser[-]	chr15@59191794	46	187			
'SLTM(NM_001013843)&SLTM(NM_024755)'	C>G	'Ala283Pro[-]&Ala301Pro[-]	chr15@59191825	42	188			
'SNCAIP(NM_005460)'	G>A	'Arg499Gln[+]'	chr5@121780331	40	168	chr5:121808230	27	97
'SNX27(NM_030918)[+]'	A>T	'None'	chr1@151664909	16	54			
'STAT3(NM_213662)'	C>T	'Gly558Asp[-]'	chr17@40475353	59	60	chr17:37728879	42	42
'SYNCRIPI(NM_006372)&SYNCRIPI(NM_001159675)'	A>T	'Ser575Thr[-]&Ser540Thr[-]	chr6@86324623	56	231			
SYNE1	C>G	Val162Leu, 155				chr6:152873139	7	70
'TBR1(NM_006593)'	G>A	'Gly128Ser[+]'	chr2@162273303	53	261			

'TEX10(NM_001161584)&TEX10(NM_017746)'	A>G	'Val232Ala[-]&Val229Ala[-]	chr9@103109183	56	201			
'TEX10(NM_001161584)&TEX10(NM_017746)'	G>C	'Leu221Val[-]&Leu218Val[-]	chr9@103109217	43	173			
'TEX10(NM_001161584)&TEX10(NM_017746)'	T>C	'Ile203Val[-]&Ile200Val[-]	chr9@103109271	29	138			
'TLR4(NM_138554)'	A>G	'Ile12Val[+]'	chr9@120466784	31	76	chr9:119506605	19	51
TMEM107	C>G	Gly140Arg				chr17:8018269	13	37
'TNFRSF13B(NM_012452)'	G>A	'Thr241Met[-]'	chr17@16843021	14	28	chr17:16783746	10	22
'TNR(NM_003285)[-]'	G>A	'None'	chr1@175365949	52	196			
'TNRC6B(NM_001162501)'	A>G	'Asn470Ser[+]'	chr22@40661643	63	234			
'TNRC6B(NM_001162501)'	T>C	'Ser465Pro[+]'	chr22@40661627	60	235			
'TNRC6B(NM_001162501)'	A>C	'Gln463Pro[+]'	chr22@40661622	58	233			
'TNRC6B(NM_001162501)'	G>C	'Glu452Asp[+]'	chr22@40661590	57	242			
'TNRC6B(NM_001162501)'	T>A	'Ser491Thr[+]'	chr22@40661705	54	239			
'TNRC6B(NM_001162501)'	C>A	'Ser491Tyr[+]'	chr22@40661706	54	245			
'TP53(NM_000546)&TP53(NM_001126117)'	C>T	'Cys141Tyr[-]&Cys9Tyr[-]'	chr17@7578508	21	21	chr17:7519233	17	17
'TRIML1(NM_178556)[+]'	T>G	'None'	chr4@189063398	12	55			
'UBE2Q2(NM_173469)&UBE2Q2(NM_001145335)'	G>A	'Ser166Asn[+]&Ser150Asn[-]	chr15@76165818	17	69			
'USP34(NM_014709)'	A>C	'Phe2756Leu[-]'	chr2@61441609	71	246			
'USP34(NM_014709)'	A>G	'Phe2756Leu[-]'	chr2@61441611	70	245			
'USP34(NM_014709)'	C>T	'Ser115Asn[-]'	chr2@61633051	33	137			
'USP34(NM_014709)'	T>C	'Asn106Ser[-]'	chr2@61633078	34	149			
'WDR20(NM_144574)'	C>A	'Pro28Gln[+]'	chr14@102606343	26	89			
'WDR64(NM_144625)'	G>T	'Val179Leu[+]'	chr1@241842838	54	209			
'WFIKKN2(NM_175575)'	C>T	'Ala208Val[+]'	chr17@48917272	40	72	chr17:46272271	30	49
'YLPM1(NM_019589)'	G>C	'Glu1358Asp[+]'	chr14@75266074	171	476			
'ZBTB26(NM_020924)'	C>G	'Cys139Ser[-]'	chr9@125681798	44	189			
'ZCCHC2(NM_017742)'	A>G	'Asn1095Ser[+]'	chr18@60242598	95	221			
'ZCCHC2(NM_017742)'	C>G	'Phe1107Leu[+]'	chr18@60242635	93	222			
'ZFHX3(NM_001164766)&ZFHX3(NM_006885)'	T>G	'Gln2705Pro[-]&Gln3619Pro[-]'	chr16@72821319	26	58			
'ZFHX3(NM_001164766)&ZFHX3(NM_006885)'	A>C	'Val2707Gly[-]&Val3621Gly[-]'	chr16@72821313	28	65			
ZFP64	T>C	Ile609Val, 555, I607				chr20:50202313	16	71
ZNF253	C>T	Arg267Stop[.]				chr19:19863855	10	87
'ZNF326(NM_182976)'	G>C	'Ser101Thr[+]'	chr1@90472996	82	396			
'ZNF417(NM_152475)'	C>T	'Arg173His[-]'	chr19@58421128	107	229			
'ZNF609(NM_015042)'	C>G	'Ser8Cys[+]'	chr15@64791641	73	207			
'ZNF792(NM_175872)'	C>G	'Gly502Ala[-]'	chr19@35449254	114	249			
'ZSCAN23(NM_001012455)'	C>T	'Cys180Tyr[-]'	chr6@28403254	33	111			

Table S7: SNVs Patient 2		Aberration		BWA/GATK Pipeline			Bowtie/In House Pipeline		
Gene	Nucleotide change	Amino acid change		Variant Reads	Total Reads	Position (hg18)	Variant Reads	Total Reads	
'ABCA13(NM_152701)'	G>A	'Val1110Ile[+]'	chr7@48312591	148	276				
'ABCC8(NM_000352)'	C>T	'Arg519His[-]'	chr11@17464341	67	136	chr11:17420917	40	83	
'AFF2(NM_001169124)&AFF2(NM_001169125)'	G>A	'Arg362Gln[+]&Arg358Gln[+]&Arg320Gln[+]'	chrX@147891443	74	74	chrX:147699135	53	53	
'ALPPL2(NM_031313)'	C>G	'Ala258Gly[+]'	chr2@233273101	14	61				
'ANKRD36(NM_001164315)'	G>A	'Gly465Arg[+]'	chr2@97827839	24	40				
'ARMC10(NM_001161012)[+]&ARMC10(NM_001161012)[-]	T>G	'None&None&None&None'	chr7@102737719	76	149				
'ARSJ(NM_024590)'	T>C	'Thr131Ala[-]'	chr4@114899600	39	112	chr4:115119049	31	84	
'BCL9(NM_004326)'	C>T	'Arg798Trp[+]'	chr1@147092353	26	69				
'BTBD7(NM_001002860)'	C>T	'Val280Ile[-]'	chr14@93760528	18	99				
'BTBD7(NM_001002860)[-]	A>G	'Ser232Pro[-]'	chr14@93760672	14	99				
'C17orf63(NM_018182)'	C>G	'Leu123Phe[-]'	chr17@27086608	15	73				
C1orf93,MMEL1	C>T	Val469Met				chr1:2517376	24	83	
'C5orf53(NM_001007189)'	C>T	'Ser13Leu[+]'	chr5@139508099	14	148				
'CCAR1(NM_018237)'	G>A	'Glu607Lys[+]'	chr10@70516223	12	93				
CCDS7771.1	A>C	Phen2220Cys				chr11:6603799	29	57	
'CELA3B(NM_007352)'	C>A	'Ala268Glu[+]'	chr1@22315762	23	30				
'CIC(NM_015125)'	G>C	'Gly939Arg[+]'	chr19@42795826	8	46				
'COL8A2(NM_005202)'	G>T	'Tyr605stop[-]'	chr1@36563467	15	59				
'DCHS1(NM_003737)'	A>C	'Phe2220Cys[-]'	chr11@6647223	47	91				
'DCUN1D1(NM_020640)'	C>T	'Arg248His[-]'	chr3@182662919	30	128	chr3:184145613	8	20	
'DUX4L6(NM_001127388)'	G>C	'Gly214Ala[+]'	chr10@135491030	82	98				
'FADS3(NM_021727)'	G>C	'Ala109Gly[-]'	chr11@61646980	8	13				
'FAM155A(NM_001080396)'	C>T	'Ala67Thr[-]'	chr13@108518746	12	88				
FLJ37453,SPEN	T>A	Met3658Lys				chr1:16138487	89	146	
'FGG(NM_000509)[-]&FGG(NM_021870)[-]	A>G	'None&None'	chr4@155533590	108	158				
'FIGN(NM_018086)'	A>T	'Ser667Thr[-]'	chr2@164466343	19	123				
'GAGE12F(NM_001098405)[+]&GAGE2D(NM_001098405)[-]	C>G	'None&None&None'	chrX@49230930	184	379				
'GCN1L1(NM_006836)'	G>C	'Ala1194Gly[-]'	chr12@120593094	19	120				
'GGT1(NM_013430)'	C>G	'Thr117Ser[+]'	chr22@25011062	10	46				
'GIGYF2(NM_001103148)&GIGYF2(NM_001103148)[-]	C>T	'Pro592Leu[+]&Pro598Leu[+]&Pro619Leu[+]'	chr2@233671354	67	197	chr2:233379598	45	112	
'GSK3A(NM_019884)'	C>A	'Val104Leu[-]'	chr19@42744268	14	90				
'GTF2IRD2(NM_173537)'	G>T	'His514Asn[-]'	chr7@74212311	26	26				
'HERC2(NM_004667)'	A>C	'Ser895Ala[-]'	chr15@28501298	13	19				
HLX	G>T	Gly396Val				chr1:219124389	7	43	

'HMCN1(NM_031935)'	C>A	'Pro2104Gln[+]'	chr1@186014826	58	149	chr1:184281449	40	92
'HOXC4(NM_014620)'	G>C	'Gly80Ala[+]'	chr12@54447945	8	77			
'HSPBAP1(NM_024610)[-]'	T>C	'None'	chr3@122478067	9	65			
'ITGB4(NM_001005731)'	A>G	'Asp303Gly[+]'	chr17@73726491	43	64	chr17:71238086	27	37
KIAA1211		Leu103Arg				chr4:56871611	23	64
'KLHDC4(NM_001184854)&KLHDC4(NM_001184854)[-]'	G>A	'Ser118Leu[-]&Ser175Leu[-]'	chr16@87764233	9	70			
'KRTAP9-2(NM_031961)'	T>A	'Cys144Ser[+]'	chr17@39383336	8	145			
'L1TD1(NM_001164835)'	G>T	'Glu409Asp[+]'	chr1@62675673	47	119			
LAS1L	A>C	Tyr115Asp				chrX:64670234	43	92
'LGALS9C(NM_001040078)'	G>A	'Arg333His[+]'	chr17@18397608	26	75			
'LIMK1(NM_002314)[+]'	C>T	'None'	chr7@73525974	12	25			
'LOC100132288(NM_001033515)'	C>T	'Val72Met[-]'	chr21@9909121	27	134			
LOC100130522,PARD6G	G>A	Ala27Val				chr18:76061799	31	55
'LRPPRC(NM_133259)'	C>A	'Arg1109Leu[-]'	chr2@44132869	8	132			
'LRRC20(NM_018205)&LRRC20(NM_018205)[-]'	C>G	'Ala108Pro[-]&Ala114Pro[-]&Ala164Phe[-]'	chr10@72061175	29	86			
'MATR3(NM_001194954)'	G>A	'Ala105Thr[+]'	chr5@138643417	42	215			
'MBD5(NM_018328)'	A>G	'Met391Val[+]'	chr2@149226683	49	209			
'MBD5(NM_018328)'	G>A	'Val426Ile[+]'	chr2@149226788	41	192			
'MBD5(NM_018328)'	G>A	'Val374Ile[+]'	chr2@149226632	33	174			
'MBD5(NM_018328)'	C>G	'Ser483Cys[+]'	chr2@149226960	16	86			
'MBD5(NM_018328)'	A>G	'Ile529Met[+]'	chr2@149227099	25	152			
'MMEL1(NM_033467)'	C>T	'Val478Met[-]'	chr1@2527516	36	145			
'MNAT1(NM_001177963)'	G>T	'Gln4His[+]'	chr14@61201592	36	105	chr14:60271345	27	75
'MUC12(NM_001164462)'	C>G	'His3330Asp[+]'	chr7@100643832	83	499			
'MUC16(NM_024690)[-]'	T>A	'None'	chr19@8997189	9	109			
'MUC5B(NM_002458)'	G>T	'Gly4047Val[+]'	chr11@1270250	37	169			
'MUC5B(NM_002458)'	G>A	'Gly4573Arg[+]'	chr11@1271827	38	464			
'NBPF1(NM_017940)'	C>G	'Val-1033Leu[-]'	chr1@16915513	13	165			
'NCAPD3(NM_015261)'	C>T	'Arg1371Gln[-]'	chr11@134027885	189	397	chr11:133533095	96	198
'NINL(NM_025176)'	T>C	'Arg948Gly[-]'	chr20@25457085	19	35			
'NLGN4Y(NM_014893)'	C>T	'Arg704Cys[+]'	chrY@16952801	82	83	chrY:15462195	53	53
'NUP98(NM_016320)&NUP98(NM_00538)'	C>G	'Arg538Pro[-]&Arg555Pro[-]'	chr11@3752738	33	168			
'OR10G9(NM_001001953)'	C>T	'Ala90Val[+]'	chr11@123893988	98	140			
'OR11H1(NM_001005239)'	G>A	'Ala252Val[-]'	chr22@16449050	277	279			
'OR11L1(NM_001001959)'	A>T	'Phe17Tyr[-]'	chr1@248005149	28	118	chr1:246071772	20	78
'OR2A1(NM_001005287)&OR2A42(NM_001005287)[-]'	C>T	'Arg74Cys[+]&Arg68Cys[+]'	chr7@144015437	480	575			
'OR2T8(NM_001005522)'	C>T	'Ala97Val[+]'	chr1@248084609	22	22			
'OVCH2(NM_198185)[-]'	A>C	'None'	chr11@7717215	8	8			

'OVCH2(NM_198185)[-]'	A>C	'None'	chr11@7717216	10	10			
'PCDH11Y(NM_032973)'	G>A	'Ala1144Thr[+]'	chrY@5605390	161	248			
'PCDHA11(NM_018902)'	G>A	'Gly514Ser[+]'	chr5@140250228	53	77			
'PCDHB5(NM_015669)'	C>T	'Thr8Met[+]'	chr5@140515039	62	137	chr5:140495223	37	87
'PKD1(NM_000296)'	C>G	'Ala3053Pro[-]'	chr16@2152426	18	86			
PLCH1						chr3:156768777	10	45
'PLXNB1(NM_002673)[-]&PLXNB1(NM_002673)'	A>G	'None&None'	chr3@48451307	11	11			
'POM121L12(NM_182595)'>	C>T	'Pro261Leu[+]'>	chr7@53104146	77	152	chr7:53071640	39	86
'PPP1CC(NM_002710)'>	C>T	'Asp210Asn[-]'>	chr12@111160396	23	176			
'PPP1CC(NM_002710)'>	C>T	'Arg188Gln[-]'>	chr12@111160461	11	138			
'PPP2R5A(NM_006243)'>	G>T	'Ser93Ile[+]'>	chr1@212502573	28	84			
'PRB1(NM_005039)'>	G>T	'Pro184Gln[-]'>	chr12@11506486	10	27			
'PRB1(NM_005039)'>	C>T	'Arg128Lys[-]'>	chr12@11506654	13	93			
'PRDM16(NM_199454)'>	G>C	'Ala367Pro[+]'>	chr1@3322125	10	35			
'PRDM2(NM_015866)&PRDM2(NM_001000)'>	A>C	'Thr702Pro[+]&Thr501Pro[+]'>	chr1@14106394	21	199			
'PRSS3(NM_007343)&PRSS3(NM_0011970)'>	C>G	'Arg255Gly[+]&Arg212Gly[+]&Arg191'>	chr9@33799026	86	379			
'PTPRK(NM_002844)&PTPRK(NM_001135)'>	G>C	'Arg1383Gly[-]&Arg1389Gly[-]'>	chr6@128294289	68	162			
'PUM1(NM_001020658)'>	C>T	'Gly734Ser[-]'>	chr1@31437644	27	222			
'PUS10(NM_144709)[-]'>	G>A	'None'>	chr2@61238892	10	42			
'RALGAPA2(NM_020343)[-]'>	T>A	'None'>	chr20@20610003	19	135			
'RALGAPA2(NM_020343)[-]'>	A>C	'None'>	chr20@20610004	18	128			
'RC3H2(NM_001100588)'>	G>T	'Pro679Gln[-]'>	chr9@125621195	35	325			
'RECQL(NM_002907)[-]&RECQL(NM_0329)'>	C>A	'None&None'>	chr12@21623284	20	39			
'RECQL(NM_002907)[-]&RECQL(NM_0329)'>	C>A	'None&None'>	chr12@21623281	10	33			
'RG9MTD2(NM_001134666)'>	G>A	'Arg69Cys[-]'>	chr4@100479349	18	76	chr4:100698372	15	51
'SCG2(NM_003469)'>	G>A	'Pro76Leu[-]'>	chr2@224463774	121	264	chr2:224172018	73	163
'SELV(NM_182704)'>	C>T	'Thr305Ile[+]'>	chr19@40009568	26	134			
'SHROOM4(NM_020717)'>	T>G	'Lys1129Gln[-]'>	chrX@50350757	14	56			
SLC2A5	G>A	Ala396Val				chr1:9020658	7	25
'SP3(NM_001172712)&SP3(NM_00101737)'>	C>A	'Glu399Asp[-]&Glu334Asp[-]&Glu402'>	chr2@174820034	12	53			
SPACA3	A>C	Ser85Arg				chr17:28346758	56	101
'SPATC1(NM_001134374)'>	T>G	'Val18Gly[+]'>	chr8@145086736	26	34			
'SPEN(NM_015001)'>	T>A	'Met3658Lys[+]'>	chr1@16265900	175	269			
'SYVN1(NM_172230)'>	T>G	'Thr328Pro[-]'>	chr11@64898255	33	40			
'TBC1D3(NM_001123391)'>	G>T	'Gln354Lys[-]'>	chr17@36339597	12	15			
'TBR1(NM_006593)'>	G>A	'Gly128Ser[+]'>	chr2@162273303	31	123			
'TUBB8(NM_177987)&TUBB8(NM_001164)'>	C>A	'Lys252Asn[-]&Lys180Asn[-]'>	chr10@93576	58	160			
'USP34(NM_014709)'>	A>C	'Phe2756Leu[-]'>	chr2@61441609	32	309			

'USP34(NM_014709)'	A>G	'Phe2756Leu[-]'	chr2@61441611	31	304			
'VCX(NM_013452)'	A>G	'Met180Val[+]'	chrX@7811974	36	271			
'VCX(NM_013452)'	G>C	'Glu159Gln[+]'	chrX@7811911	42	346			
'WASH1(NM_182905)'	G>C	'Pro303Ala[-]'	chr9@16853	14	25			
'YTHDF3(NM_152758)'	G>A	'Arg528Gln[+]'	chr8@64100153	38	298			
'YTHDF3(NM_152758)'	G>A	'Gly137Glu[+]'	chr8@64098980	32	341			
'ZFHX3(NM_001164766)&ZFHX3(NM_00681)'>	A>C	'Val2707Gly[-]&Val3621Gly[-]'>	chr16@72821313	14	66			
'ZFHX3(NM_001164766)&ZFHX3(NM_00681)'>	T>G	'Gln2705Pro[-]&Gln3619Pro[-]'>	chr16@72821319	11	61			
'ZFHX4(NM_024721)'	G>A	'Met38Ile[+]'>	chr8@77616437	39	319			
'ZFHX4(NM_024721)'	C>T	'Thr24Met[+]'>	chr8@77616394	27	238			
'ZNF235(NM_004234)'	G>A	'Arg479stop[-]'>	chr19@44792153	48	194	chr19:49483993	36	119
'ZNF322B(NM_199005)'	G>T	'Pro22Thr[-]'>	chr9@99961730	79	184			
'ZNF326(NM_182976)'	G>C	'Ser101Thr[+]'>	chr1@90472996	30	246			
'ZNF326(NM_182976)[+]'	C>T	'None'>	chr1@90472900	28	183			
'ZNF609(NM_015042)'	C>G	'Ser8Cys[+]'>	chr15@64791641	46	181			
'ZNF717(NM_001128223)'	G>T	'Leu300Ile[-]'>	chr3@75787876	8	20			
'ZNF75A(NM_153028)'	G>C	'Glu158Asp[+]'>	chr16@3367452	54	141	chr16:3307453	37	94

Table S8: SNVs Patient 3		Aberration		BWA/GATK Pipeline			Bowtie/In House Pipeline		
Gene	Nucleotide change	Amino acid change		Position (hg19)	Variant reads	Total reads	Posiiton (hg18)	Variant reads	Total reads
'ABCA8(NM_007168)'	G>A	'Arg1421Trp[-]'		chr17@66871864	32	106	chr17:64383459	22	69
'ACTBL2(NM_001017992)'	G>A	'Arg117Trp[-]'		chr5@56778186	33	187	chr5:56813943	25	114
'ADAMTS4(NM_005099)'	C>T	'Arg290His[-]'		chr1@161166435	23	114	chr1:159433059	20	81
ADHFE1	C>T	Arg288Trp					chr8:67526869	25	137
'AGPHD1(NM_001013619)'	C>G	'Leu12Val[+]'		chr15@78805464	28	143	chr15:76592519	20	92
'AGRN(NM_198576)'	G>A	'Arg1656Gln[+]'		chr1@985700	28	44			
'APLP1(NM_001024807)&APLP1(NM_005166)'	C>T	'Arg605Cys[+]&Arg604Cys[+]'		chr19@36370075	20	74	chr19:41061915	15	54
'ARHGAP31(NM_020754)'	C>A	'Pro1098Gln[+]'		chr3@119134069	48	194	chr3:120616759	37	116
ASPDH	C>T	Val156Ile, Val261Ile					chr19:55707232	8	12
'ASPM(NM_018136)'	T>G	'Lys2171Thr[-]'		chr1@197071869	62	179	chr1:195338492	42	119
'ATP1B4(NM_001142447)'	C>T	'Arg44Trp[+]'		chrX@119500446	183	241	chrX:119384474	93	134
'AUP1(NM_181575)'	G>A	'Thr98Ile[-]'		chr2@74756305	20	185	chr2:74609813	14	107
AURKA	A>G	Trp313Arg					chr20:54379040	55	161
'BHLHB9(NM_001142528)'	T>G	'Asn209Lys[+]'		chrX@102004550	19	58	chrX:101891206	16	46
'BNC2(NM_017637)'	G>A	'Arg698Trp[-]'		chr9@16436100	101	181	chr9:16426100	60	109
'BTNL8(NM_001159709)&BTNL8(NM_00104046)	T>G	'His186Gln[+]&His311Gln[+]&His195Gln[+]'		chr5@180376974	261	261			
'BTNL8(NM_001159709)&BTNL8(NM_00104046)	C>G	'His186Asp[+]&His311Asp[+]&His195Asp[+]'		chr5@180376972	258	259			
'C19orf51(NM_178837)'	C>A	'Arg121Met[-]'		chr19@55677233	18	73	chr19:60369045	11	49
'C19orf51(NM_178837)'	T>C	'Arg121Gly[-]'		chr19@55677234	19	74	chr19:60369046	12	48
'CA7(NM_005182)[+]&CA7(NM_001014435)[+]'	C>T	'None&None'		chr16@66885360	56	324			
'CACNA1E(NM_000721)'	G>A	'Val65Ile[+]'		chr1@181453073	18	71			
'CACNA1E(NM_000721)'	C>T	'Ala1445Val[+]'		chr1@181727087	21	131			
'CCDC129(NM_194300)'	C>A	'Arg201Ser[+]'		chr7@31617479	36	137	chr7:31584004	26	90
'CCDC144A(NM_014695)'	G>A	'Glu1209Lys[+]'		chr17@16664991	102	240			
'CCDC152(NM_001134848)'	G>A	'Glu238Lys[+]'		chr5@42799830	31	160	chr5:42835587	19	94
'CCDC89(NM_152723)'	G>A	'Ala291Val[-]'		chr11@85396302	48	231	chr11:85073950	36	141
CCDS43129.1,TMPRSS7	C>G	Pro447Ala, Pro592Ala					chr3:113278609	30	128
CCR3(NM_001837)&CCR3(NM_178328)&CCR3(NM_001014435)	C>T	'Leu260Phe[+]&Leu281Phe[+]&Leu278Phe[+]'		chr3@46307427	37	169	chr3:46282431	30	115
'CDC42BPB(NM_006035)'	G>A	'Ser244Leu[-]'		chr14@103450053	43	142	chr14:102519806	28	86
CDH9	T>C	Ile131Val					chr5:26951627	14	118
'CHD7(NM_017780)'	A>G	'Lys928Glu[+]'		chr8@61734433	44	542	chr8:61896987	35	179
'CHD9(NM_025134)'	C>G	'Ser23stop[+]'		chr16@53190069	51	209	chr16:51747570	33	126
CLPS	G>T	Leu71Ile					chr6:35871029	17	97
'CLPTM1(NM_001199468)'	A>G	'Tyr133Cys[+]'		chr19@45477784	38	170	chr19:50169624	31	106
'CNGA1(NM_001142564)&CNGA1(NM_000087)'	G>C	'Thr87Ser[-]&Thr18Ser[-]'		chr4@47954666	61	259	chr4:47649423	41	142

CNKS2	G>A	Arg806Gln				chrX:21537381	6	52
'CNTNAP3(NM_033655)'	C>A	'Gly714Val[-]'	chr9@39118196	222	222			
'COL3A1(NM_000090)'	C>T	'Arg449Cys[+]'	chr2@189859318	50	257	chr2:189567563	35	138
'COL4A5(NM_000495)'	C>G	'Pro1272Ala[+]'	chrX@107920753	34	70	chrX:107807409	22	47
'CPT1B(NM_001145134)&CPT1B(NM_004377) &	G>A	'Arg661Cys[-]&Arg695Cys[-]&Arg614Cys[-]'	chr22@51008781	23	103	chr22:49355647	18	72
CYP2C19	G>A	Arg132Gln				chr10:96525200	50	125
'DNAH5(NM_001369)'	C>T	'Arg956His[-]'	chr5@13885214	101	217	chr5:13938214	67	141
'DNAH5(NM_001369)'	G>C	'Ser2605stop[-]'	chr5@13807773	44	337	chr5:13860773	31	148
'EIF5AL1(NM_001099692)'	G>C	'Val137Leu[+]'	chr10@81272814	154	364			
'FAM120B(NM_032448)'	G>A	'Arg399Gln[+]'	chr6@170627674	73	552			
'FAM184B(NM_015688)'	G>A	'Arg523Cys[-]'	chr4@17690076	54	258	chr4:17299174	35	137
'FAM5C(NM_199051)'	G>T	'Ser744Tyr[-]'	chr1@190067218	28	190	chr1:188333841	23	115
'FAM83H(NM_198488)'	C>A	'Val429Leu[-]'	chr8@144810346	34	41			
FAS	C>A	Thr214Asn, Thr193Asn				chr10:90761808	29	113
'FAT2(NM_001447)'	C>T	'Arg308Gln[-]'	chr5@150947570	30	150	chr5:15092776	22	94
'FBXW10(NM_031456)'	G>T	'Arg275Leu[+]'	chr17@18653188	29	160			
'FRG2C(NM_001124759)'	A>G	'Glu166Gly[+]'	chr3@75714840	597	989			
'FRG2C(NM_001124759)'	G>T	'Asp109Tyr[+]'	chr3@75714345	524	1000			
FSD1L	G>A	Arg350Gln, Arg318Gln				chr9:107336618	12	75
GCNT2	G>C	Gly261Arg				chr6:10665423	27	98
'GDPD5(NM_030792)'	G>A	'Arg526Trp[-]'	chr11@75148074	57	74	chr11:74825722	38	49
'GEMIN5(NM_015465)'	A>G	'Val56Ala[-]'	chr5@154316745	147	198	chr5:154296938	67	97
'GPR158(NM_020752)'	C>T	'Thr514Met[+]'	chr10@25861604	117	560	chr10:25901610	50	179
'GRIA4(NM_001077243)'	C>A	'Thr421Lys[+]'	chr11@105781264	25	314	chr11:105286474	13	127
'HECTD2(NM_182765)'	T>C	'Tyr155His[+]'	chr10@93221066	44	170	chr10:93211046	33	102
'HECW1(NM_015052)'	G>A	'Glu729Lys[+]'	chr7@43484956	12	53		33	102
'HGF(NM_001010932)&HGF(NM_000601)'	G>T	'Pro695Gln[-]&Pro700Gln[-]'	chr7@81331985	72	316	chr7:81169921	46	155
'HJURP(NM_018410)'	C>G	'Arg403Thr[-]'	chr2@234750218	56	216	chr2:234414957	42	133
'HLA-DRB1(NM_002124)'	A>T	'Cys11Ser[-]'	chr6@32557489	65	225			
'HMCN1(NM_031935)'	C>T	'Arg2742stop[+]'	chr1@186043957	30	254	chr1:184310580	26	121
HOXD8	T>G	Phe148Leu				chr2:176703784	7	40
'HP(NM_001126102)&HP(NM_005143)'	C>T	'Ala296Val[+]&Ala355Val[+]'	chr16@72094632	108	546	chr16:70652133	61	196
'HYDIN(NM_032821)'	G>C	'Ser3894Cys[-]'	chr16@70896044	52	421			
'IGSF3(NM_001542)&IGSF3(NM_001007237)'	A>G	'Ile639Thr[-]&Ile619Thr[-]'	chr1@117142736	187	294			
'INO80D(NM_017759)'	C>A	'Gly672Val[-]'	chr2@206870161	39	234	chr2:206578406	28	122
'KIAA1109(NM_015312)'	G>T	'Glu3514stop[+]'	chr4@123237887	61	152	chr4:123457337	44	91
'KLHL1(NM_020866)'	C>G	'Glu415Gln[-]'	chr13@70413279	70	380	chr13:69311280	43	147
'KRTAP4-9(NM_001146041)'	G>A	'Arg161His[+]'	chr17@39262122	107	152			

'LCT(NM_002299)'	A>G	'Phe1322Ser[-]'	chr2@136564906	34	170	chr2:136281376	24	101
'LILRB3(NM_001081450)'	C>T	'Ala4Thr[-]'	chr19@54726839	42	139			
'LIMS1(NM_001193483)&LIMS1(NM_004987)&L	G>A	'Gly28Ser[+]&Gly16Ser[+]&Gly20Ser[+]	chr2@109276110	142	259			
'LMF1(NM_022773)'	C>T	'Arg461His[-]'	chr16@919917	29	116	chr16:859918	14	58
'LONRF3(NM_001031855)'	C>A	'Pro54Thr[+]'	chrX@118108903	14	18	chrX:117992931	10	14
'LRP2(NM_004525)'	G>T	'Leu433Ile[-]'	chr2@169999295	62	340	chr2:169707541	45	170
'LRRK1(NM_024652)'	A>T	'Asn556Ile[+]'	chr15@101561315	49	185	chr15:99378838	34	115
'MAB21L2(NM_006439)'	C>T	'Gln169stop[+]'	chr4@151504686	12	43	chr4:151724136	11	35
'MACF1(NM_012090)&MACF1(NM_033044)'	G>A	'Ala5147Thr[+]&Ala5649Thr[+]'	chr1@39927647	50	326	chr1:39700234	20	105
'MAGEB6(NM_173523)'	G>A	'Arg46His[+]'	chrX@26212100	78	103	chrX:26122021	48	66
'MARCO(NM_006770)'	G>A	'Ala344Thr[+]'	chr2@119739953	228	578	chr2:119456423	110	206
'MPP3(NM_001932)[-]'	C>A	'None'	chr17@41901291	73	259			
MRPS15	A>G	Val88Ala				chr1:36699489	13	83
'MUC12(NM_001164462)'	A>C	'Asn4290His[+]'	chr7@100646712	135	510			
'MUC12(NM_001164462)'	C>G	'Thr294Ser[+]'	chr7@100634725	119	598			
'MUC12(NM_001164462)'	C>T	'Thr4327Ile[+]'	chr7@100646824	162	1000			
'MUC17(NM_001040105)'	G>A	'Arg903His[+]'	chr7@100677405	149	807			
'MUC4(NM_018406)'	G>A	'Leu3542Phe[-]'	chr3@195507827	289	943			
'MUC4(NM_018406)'	A>G	'Val1145Ala[-]'	chr3@195515017	89	642			
'MUC4(NM_018406)'	G>T	'Leu1105Ile[-]'	chr3@195515138	121	780			
'MUC5B(NM_002458)'	G>C	'Arg2211Pro[+]'	chr11@1264742	161	161			
'MUC5B(NM_002458)'	C>T	'Thr3763Ile[+]'	chr11@1269398	142	151			
'MUC6(NM_005961)'	G>T	'Thr2023Lys[-]'	chr11@1016733	100	1000			
MYH11	A>G	Val1527Ala, Val1534Ala				chr16:15722408	12	45
'MYOM2(NM_003970)'	G>A	'Arg1033His[+]'	chr8@2057240	50	123	chr8:2044647	37	89
'NBPF1(NM_017940)'	G>A	'Thr-102Met[-]'	chr1@16891365	14	128			
'NCAM2(NM_004540)'	G>A	'Arg77Gln[+]'	chr21@22656613	71	180	chr21:21578484	39	98
NLGN4X	A>C	Leu773Arg				chrX:5820991	92	210
'NR3C1(NM_001020825)&NR3C1(NM_00102409)	C>T	'Gly609Glu[-]&Gly610Glu[-]'	chr5@142678299	46	180	chr5:142658492	31	105
'NRAS(NM_002524)'	T>A	'Gln61Leu[-]'	chr1@115256529	53	145	chr1:115058052	39	96
'OR51T1(NM_001004759)'	T>C	'Tyr209His[+]'	chr11@4903673	8	251			
'PAPPA(NM_002581)'	G>A	'Arg1609Gln[+]'	chr9@119158837	17	125	chr9:118198658	9	72
'PAPPA(NM_002581)'	G>T	'Trp1067Leu[+]'	chr9@119093575	49	162	chr9:118133396	30	99
PAPPA	T>G	Trp1067Gly				chr9:118133395	30	98
'PCBP1(NM_006196)'	T>A	'Leu100Gln[+]'	chr2@70315174	20	73	chr2:70168678	8	46
PCDHGA12	G>A	Glu358Lys				chr5:140791582	6	19
'PCNT(NM_006031)'	G>A	'Val161Ile[+]'	chr21@47754524	24	223			
'PDE4DIP(NM_001198834)&PDE4DIP(NM_001198834)'	C>T	'Ala167Thr[-]&Ala233Thr[-]&Ala135Thr[-]'	chr1@144952220	151	336			

'PDPR(NM_017990)[+]'	G>T	'None'	chr16@70161159	135	235				
'PDZD2(NM_178140)'	C>T	'Arg331stop[+]'	chr5@31995694	71	394	chr5:32031451	41	157	
'PHF3(NM_015153)'	T>C	'Leu56Pro[+]'	chr6@64356623	26	124	chr6:64414582	16	63	
'PLTP(NM_006227)&PLTP(NM_182676)'	C>T	'Arg372His[-]&Arg320His[-]'	chr20@44530966	8	69	chr20:43964373	6	51	
'POTEC(NM_001137671)'	G>C	'Ser337Cys[-]'	chr18@14533105	518	518				
'PRDM9(NM_020227)[+]'	A>T	'None'	chr5@23510142	15	179				
'PRKCG(NM_002739)'	G>A	'Val583Met[+]'	chr19@54407979	16	95	chr19:5909979	11	53	
'PSG1(NM_001184826)'	C>T	'Arg288Gln[-]'	chr19@43373033	168	461				
'PTCHD3(NM_001034842)'	G>T	'Gln253Lys[-]'	chr10@27702423	27	130				
'RABL2A(NM_007082)'	G>A	'Arg82Gln[+]'	chr2@114392655	111	239				
'RBM20(NM_001134363)'	G>A	'Gly295Arg[+]'	chr10@112541250	24	94	chr10:112531240	17	66	
'SFMBT2(NM_001029880)'	G>A	'Ala391Val[-]'	chr10@7269848	12	69	chr10:7309854	9	45	
'SFTPД(NM_003019)'	C>A	'Gly70Val[-]'	chr10@81702626	21	73	chr10:81692606	14	51	
'SKA1(NM_001039535)'	C>T	'Pro96Leu[+]'	chr18@47908572	50	153	chr18:46162570	37	103	
'SLC13A2(NM_003984)&SLC13A2(NM_00114597)	G>A	'Ala460Thr[+]&Ala417Thr[+]&Ala509Th	chr17@26822742	11	60	chr17:23846869	9	49	
SLC25A38	C>G	Tyr109Stop				chr3:39407986	14	94	
'SLC50A1(NM_001122839)'	A>G	'Tyr83Cys[+]'	chr1@155109393	22	119	chr1:153376017	16	73	
'SNTG1(NM_018967)'	T>A	'Phe318Ile[+]'	chr8@51569571	33	163	chr8:51732124	26	94	
SPG20	T>A	Lys362Asn				chr13:35801577	61	225	
'STEAP2(NM_152999)'	T>A	'Phe393Leu[+]'	chr7@89859344	53	289	chr7:89697280	36	136	
'SUN3(NM_001030019)'	C>T	'Glu269Lys[-]'	chr7@48033968	37	366	chr7:48000493	27	157	
'TCEB3CL(NM_001100817)'	G>A	'Ser361Leu[-]'	chr18@44543290	76	282				
'TEX13B(NM_031273)'	G>A	'Pro292Leu[-]'	chrX@107224374	59	162	chrX:107111030	37	97	
'TGM2(NM_004613)'	G>A	'Ala145Val[-]'	chr20@36779459	17	192	chr20:36212873	7	59	
'TLE4(NM_007005)'	G>C	'Arg500Thr[+]'	chr9@82333795	49	207	chr9:81523615	33	123	
'TMEM131(NM_015348)'	A>C	'Ser156Ala[-]'	chr2@98475784	36	168	chr2:97842216	26	100	
'TP53(NM_000546)&TP53(NM_001126117)'	C>T	'Arg175His[-]&Arg43His[-]'	chr17@7578406	82	111	chr17:7519131	56	80	
'TPRX1(NM_198479)'	A>G	'Ser244Pro[-]'	chr19@48305538	29	179				
'TPTE(NM_199261)'	C>T	'Gly18Ser[-]'	chr21@10971305	48	333	chr21:9993176	34	150	
'TRIM42(NM_152616)'	G>C	'Val551Leu[+]'	chr3@140407175	24	111	chr3:141889865	14	73	
'TRPV3(NM_145068)'	C>T	'Asp340Asn[-]'	chr17@3435998	51	67	chr17:3382748	36	50	
'TTC35(NM_014673)'	G>C	'Gly49Ala[+]'	chr8@109462157	49	476	chr8:109531333	35	145	
'UNC80(NM_032504)&UNC80(NM_182587)'	G>T	'Arg2065Leu[+]&Arg2060Leu[+]'	chr2@210802281	90	413	chr2:210510526	55	183	
'USE1(NM_018467)'	G>A	'Arg122Gln[+]'	chr19@17327111	10	32	chr19:17188111	8	24	
'VPS13A(NM_033305)'	A>C	'Asp170Ala[+]'	chr9@79825545	30	125	chr9:79015365	24	90	
'VRK2(NM_001130480)[+]&VRK2(NM_001130484)'	G>T	'None&None&None&None&None'	chr2@58315475	78	232				
'VWF(NM_000552)'	C>T	'Val456Met[-]'	chr12@6173478	12	64	chr12:6043739	9	43	
'WFS1(NM_001145853)'	C>A	'Pro216Thr[+]'	chr4@6293658	9	39	chr4:6344559	8	30	



Table S9: SNVs Patient 4

Gene	Aberration		BWA/GATK Pipeline			Bowtie/In House Pipeline		
	Nucleotide change	Amino acid change	Position (hg19)	Variant Reads	Total Reads	Position (hg18)	Variant Reads	Total Reads
'ACTR5(NM_024855)'	G>A	'Val433Met[+]'	chr20@37394884	125	259	chr20:36828298	71	152
'ANGPTL7(NM_021146)'	C>T	'Arg289Cys[+]'	chr1@11254710	42	150	chr1:11177297	33	99
'ANO2(NM_020373)'	G>A	'Arg155Trp[-]'	chr12@6030265	68	239	chr12:5900526	45	135
'C22orf39(NM_173793)'	G>A	'Arg111stop[-]'	chr22@19431886	10	44			
CCDS33599.1	G>A	Arg72stop				chr22:17811886	7	33
'CXorf30(NM_001098843)'	G>T	'Glu533stop[+]'	chrX@36397538	67	313			
'DNM2(NM_001190716)&DNM2(	A>T	'Glu540Val[+]&Glu536Val[+]'	chr19@10923001	21	111	chr19:10784001	15	71
'EIF4A3(NM_014740)'	C>G	'Gly309Ala[-]'	chr17@78111242	111	304	chr17:75725837	64	171
'ELK1(NM_005229)'	G>A	'Arg74Cys[-]'	chrX@47498728	18	48	chrX:47383672	14	35
'EPB41L2(NM_001431)'	C>G	'Asp357His[-]'	chr6@131222181	55	232	chr6:131263874	40	133
'FREM1(NM_144966)'	A>G	'Val480Ala[-]'	chr9@14842613	42	145	chr9:14832613	27	81
GABRG3	A>G	Thr390Ala				chr15:25451386	47	174
GPR107	C>G	Leu120Val				chr9:131879450	37	124
'GRIA3(NM_007325)'	T>A	'Phe547Leu[+]'	chrX@122551393	118	542			
'HGC6.3(NM_001129895)'	T>G	'Gln151Pro[-]'	chr6@168376881	24	167			
'HIAT1(NM_033055)[+]'	C>T	'None'	chr1@100542718	11	107			
'HRAS(NM_001130442)'	T>A	'Gln61Leu[-]'	chr11@533874	46	85	chr11:523874	30	53
'IGFN1(NM_001164586)'	C>T	'Ala1572Val[+]'	chr1@201178736	120	969			
KRT76	G>T	Tyr613Stop				chr12:51448842	6	58
'KIF6(NM_145027)[-]'	G>T	'None'	chr6@39311595	37	158			
'LOC100132247(NM_001135865)	G>C	'Ala521Pro[+]'	chr16@22545865	29	172			
'LOC729991(NM_001145784)'	A>T	'Trp56Arg[-]'	chr19@19296892	11	61	chr19:19157892	7	45
'MLL3(NM_170606)'	A>G	'Tyr987His[-]'	chr7@151927025	79	441			
'MUC4(NM_018406)'	G>A	'Pro3664Ser[-]'	chr3@195507461	152	431			
'PLCB1(NM_182734)'	G>A	'Ser236Asn[+]'	chr20@8639196	58	174	chr20:8587196	37	106
'PNLDC1(NM_173516)'	C>A	'Thr297Lys[+]'	chr6@160232802	38	204	chr6:160152792	25	113
'PPBP(NM_002704)'	C>T	'Glu93Lys[-]'	chr4@74853241	72	344	chr4:75072105	49	178
'RAB11FIP2(NM_014904)'	G>A	'Ala309Val[-]'	chr10@119798822	113	363	chr10:119788812	67	188
SRSF10	T>C					chr1:24170398	75	214
'ST6GALNAC2(NM_006456)'	C>G	'Lys205Asn[-]'	chr17@74568773	46	201	chr17:72080368	29	111
'SUGT1(NM_001130912)&SUGT	A>G	'Lys363Glu[+]&Lys331Glu[+]'	chr13@53261959	51	173	chr13:52159960	30	82
'TARBP2(NM_134323)&TARBP2	A>G	'Thr132Ala[+]&Thr111Ala[+]'	chr12@53897564	23	81	chr12:52183831	14	59
'TEX15(NM_031271)'	C>A	'Asp134Tyr[-]'	chr8@30706134	35	142	chr8:30825676	26	94
'TSPAN4(NM_001025239)&TSPA	A>G	'Asn88Ser[+]&Asn152Ser[+]'	chr11@865716	19	101	chr11:855716	16	71

'WNK3(NM_001002838)'	A>G	'Ser477Pro[-]'	chrX@54321250	20	111	chrX:54337975	16	67
'ZNF678(NM_178549)'	A>C	'Lys374Asn[+]'	chr1@227842908	33	91			

Table S10: Germline Patient 3

Gene	Chr	Position	Mutation	Variant Reads	Total Reads	AA Change	HMGD
'ABCA13(NM_152701)'	chr7	48349595	A>G	84	110	'Ile3125Val[+]'	No
'ABCG8(NM_022437)'	chr2	44099233	G>A	74	96	'Trp361stop[+]'	No
'ABHD12B(NM_181814)&ABHD12B(NM_181533)'	chr14	51368610	A>G	52	70	'Ile205Val[+]&Ile175Val[+]'	No
'ACAN(NM_001135)'	chr15	89399986	C>G	36	10	'Asp1390Glu[+]'	No
'ADAM2(NM_001464)'	chr8	39604116	T>A	82	90	'Lys683Asn[-]'	No
'ADAMTS5(NM_007038)'	chr21	28338031	T>A	12	14	'Asn227Ile[-]'	No
'ADAT1(NM_012091)'	chr16	75646442	G>A	62	106	'Pro248Ser[-]'	No
'ADCY3(NM_004036)'	chr2	25061464	C>T	30	24	'Met461Ile[-]'	No
'AHNAK(NM_001620)'	chr11	62293925	C>A	118	126	'Gly2655Val[-]'	No
'AHNAK(NM_001620)'	chr11	62290857	G>C	122	132	'Leu3678Val[-]'	No
'AIF1L(NM_001185095)&AIF1L(NM_001185096)'	chr9	133989973	T>C	138	116	'Met83Thr[+]&Met57Thr[+]'	No
'ALG1(NM_019109)'	chr16	5132586	C>G	12	128	'His367Asp[+]'	No
'ALPK3(NM_020778)'	chr15	85366575	G>A	132	84	'Arg255Gln[+]'	No
'ANK2(NM_001127493)[+]&ANK2(NM_001148)[+]&A'	chr4	114214588	C>T	136	128	'Not Det&Not Det&Not Det'	No
'ANKRD36(NM_001164315)'	chr2	97827839	G>A	68	22	'Gly465Arg[+]'	No
'ANKRD36(NM_001164315)[+]'	chr2	97827830	T>A	14	94	'Not Det'	No
'AP1S3(NM_001039569)'	chr2	224642493	G>A	76	86	'Arg33Trp[-]'	No
'AQP12B(NM_001102467)'	chr2	241622034	G>C	36	62	'Thr74Ser[-]'	No
'ARHGAP11A(NM_014783)'	chr15	32921855	G>C	98	114	'Asp333His[+]'	No
'ARHGAP4(NM_001666)[-]&ARHGAP4(NM_00116474)	chrX	153173422	G>A	14	0	'Not Det&Not Det'	No
'ARSH(NM_001011719)'	chrX	2933233	G>A	186	0	'Arg188His[+]'	No
'ASCC1(NM_001198798)'	chr10	73970584	T>C	68	64	'Met40Val[-]'	No
'ASH1L(NM_018489)'	chr1	155408815	C>G	42	44	'Asp1711His[-]'	No
'ASPDH(NM_001024656)&ASPDH(NM_001114598)'	chr19	51015420	C>T	16	34	'Val156Ile[-]&Val261Ile[-]'	No
'ATAD5(NM_024857)'	chr17	29162598	C>T	70	74	'Thr500Ile[+]'	No
'ATG9A(NM_024085)'	chr2	220088694	C>T	70	60	'Arg439His[-]'	No
'ATM(NM_000051)'	chr11	108186821	G>A	98	78	'Arg2060His[+]'	No
'ATP13A5(NM_198505)'	chr3	193052747	C>G	66	80	'Gly362Ala[-]'	No

'ATP1A4(NM_144699)'	chr1	160141491	C>T	64	64	'Pro600Ser[+]' No
'ATP7A(NM_000052)'	chrX	77294387	A>G	98	0	'Ile1189Val[+]' No
'ATRIP(NM_130384)&ATRIP(NM_032166)'	chr3	48506291	G>T	44	44	'Gly706Val[+]&Gly679Val[+]' No
'AUP1(NM_181575)'	chr2	74754075	C>T	74	82	'Ala397Thr[-]' No
'AZU1(NM_001700)[+]'	chr19	829555	C>G	20	38	'Not Det' No
'BAP1(NM_004656)[-]'	chr3	52436441	C>A	42	42	'Not Det' No
'BAT2L2(NM_015172)'	chr1	171510753	A>T	26	22	'Glu1381Val[+]' No
'BCAT2(NM_001190)'	chr19	49309937	T>C	72	66	'His46Arg[-]' No
'BIRC6(NM_016252)'	chr2	32740648	T>G	40	42	'Cys3720Trp[+]' No
'BMPR2(NM_001204)'	chr2	203383561	G>A	82	104	'Arg213Gln[+]' No
'BOD1L(NM_148894)'	chr4	13602229	G>C	52	64	'Leu2099Val[-]' No
'BRD1(NM_014577)'	chr22	50192748	A>G	42	38	'Met515Thr[-]' No
'BRD2(NM_005104)'	chr6	32942318	T>A	60	44	'Ser37Thr[+]' No
'BTN3A1(NM_001145008)&BTN3A1(NM_007048)'	chr6	26408145	T>A	112	110	'Leu175His[+]&Leu227His[+]' No
'C14orf143(NM_145231)'	chr14	90420250	C>A	76	84	'Lys57Asn[-]' No
'C1orf127(NM_001170754)'	chr1	11009716	C>G	80	78	'Asp419His[-]' No
'C20orf132(NM_152503)&C20orf132(NM_213632)'	chr20	35772133	A>G	80	80	'Phe-602Ser[-]&Phe-158Ser[-]' No
'C22orf30(NM_173566)'	chr22	32111642	G>A	74	110	'Ser728Leu[-]' No
'C2orf67(NM_152519)'	chr2	211018643	C>T	62	86	'Ala222Thr[-]' No
'C5orf42(NM_023073)'	chr5	37206317	C>T	66	74	'Arg1044His[-]' No
'C5orf60(NM_001142306)'	chr5	179071925	G>A	32	120	'Pro33Ser[-]' No
'C7orf43(NM_018275)'	chr7	99755792	C>A	20	14	'Gly111Trp[-]' No
'C7orf43(NM_018275)'	chr7	99754568	C>G	68	78	'Gly298Ala[-]' No
'C9orf174(NM_020893)'	chr9	100105679	A>G	72	88	'Thr822Ala[+]' No
'CACHD1(NM_020925)'	chr1	65124398	C>T	82	64	'Thr547Ile[+]' No
'CACNA1G(NM_198397)'	chr17	48683583	T>C	26	22	'Ser1541Pro[+]' No
'CBR3(NM_001236)'	chr21	37510213	C>T	118	76	'Pro127Leu[+]' No
'CCDC157(NM_001017437)'	chr22	30772424	C>T	66	64	'Pro650Leu[+]' No
'CCDC74A(NM_138770)'	chr2	132288314	C>T	48	84	'Ala153Val[+]' No
'CCDC87(NM_018219)'	chr11	66359489	C>T	38	22	'Arg333His[-]' No

'CDC27(NM_001114091)'	chr17	45234417	A>G	120	100	'Ile235Thr[-]'	No
'CDC27(NM_001114091)&CDC27(NM_001256)'	chr17	45214564	A>T	68	136	'Cys629Ser[-]&Cys623Ser[-]'	No
'CDC27(NM_001114091)&CDC27(NM_001256)'	chr17	45219311	T>C	26	116	'Ile493Val[-]&Ile487Val[-]'	No
'CDC27(NM_001114091)&CDC27(NM_001256)'	chr17	45214636	T>C	16	152	'Asn605Asp[-]&Asn599Asp[-]'	No
'CDH15(NM_004933)[+]'	chr16	89253972	C>T	32	56	Not Det'	No
'CDK10(NM_052988)&CDK10(NM_001098533)'	chr16	89761077	G>A	12	12	'Val225Met[+]&Val154Met[+]'	No
'CDK17(NM_002595)'	chr12	96707125	G>A	48	46	'Arg131Cys[-]'	No
'CDKL3(NM_001113575)'	chr5	133642326	T>C	58	78	'Arg478Gly[-]'	No
'CELSR1(NM_014246)'	chr22	46793621	T>C	46	82	'Asn1884Ser[-]'	No
'CENPN(NM_001100624)'	chr16	81060197	C>T	84	82	'Thr255Ile[+]'	No
'CHM(NM_000390)'	chrX	85233820	T>A	128	0	'Ser89Cys[-]'	No
'CHP(NM_007236)[+]'	chr15	41570961	C>T	68	84	Not Det'	No
'CIITA(NM_000246)'	chr16	11000940	G>A	8	8	'Gly531Ser[+]'	No
'CLEC17A(NM_207390)[+]'	chr19	14707903	C>G	138	162	Not Det'	No
'CLTCL1(NM_007098)[-]&CLTCL1(NM_001835)[-]'	chr22	19184171	G>C	22	38	Not Det&Not Det'	No
'CLVS2(NM_001010852)'	chr6	123332273	G>A	62	68	'Ser178Asn[+]'	No
'COL23A1(NM_173465)'	chr5	177683382	C>T	22	8	'Arg285Gln[-]'	No
'COL23A1(NM_173465)'	chr5	177733908	C>T	34	30	'Arg125Gln[-]'	No
'CORO2B(NM_006091)&CORO2B(NM_001190456)'	chr15	69003978	T>A	44	34	'Leu194Gln[+]&Leu189Gln[+]'	No
'CPNE2(NM_152727)[+]'	chr16	57153567	G>A	30	24	Not Det'	No
'CRMP1(NM_001313)&CRMP1(NM_001014809)'	chr4	5830233	C>T	52	44	'Val482Ile[-]&Val596Ile[-]'	No
'CRX(NM_000554)'	chr19	48342757	C>T	30	32	'Pro145Ser[+]'	No
'CST9(NM_001008693)'	chr20	23586366	T>C	80	68	'Met46Val[-]'	No
'CTBP2(NM_022802)'	chr10	126715970	A>T	26	30	'Val120Glu[-]'	No
'CUTA(NM_001014433)'	chr6	33385887	A>G	52	66	'Ser26Pro[-]'	No
'CYP2C19(NM_000769)'	chr10	96535294	A>G	96	142	'Lys160Arg[+]'	No
'DCC(NM_005215)'	chr18	50450122	A>T	52	62	'Asn248Ile[+]'	No
'DEPDC6(NM_022783)'	chr8	120942167	G>T	64	108	'Arg138Ser[+]'	No
'DGKG(NM_001346)&DGKG(NM_001080744)&DGKG'	chr3	185960347	A>G	60	80	'Ile591Thr[-]&Ile566Thr[-]&Ile551Val[-]'	No
'DHX34(NM_014681)'	chr19	47879778	G>A	10	16	'Ala854Thr[+]'	No

'DMKN(NM_033317)'	chr19	36002711	G>A	118	146	'Thr230Met[-]'	No
'DNAH12(NM_178504)[-]'	chr3	57431752	T>A	44	0	'Not Det'	No
'DNHD1(NM_144666)'	chr11	6584223	G>A	54	36	'Met3177Ile[+]'	No
'DNM2(NM_001190716)'	chr19	10887881	C>T	58	88	'Pro226Leu[+]'	No
'DOCK1(NM_001380)'	chr10	129224153	G>A	82	40	'Glu1577Lys[+]'	No
'DOCK4(NM_014705)'	chr7	111629218	G>A	44	56	'Arg106Cys[-]'	No
'DONSON(NM_017613)'	chr21	34954318	A>G	88	114	'Trp364Arg[-]'	No
'DSC1(NM_024421)'	chr18	28721967	C>G	118	98	'Val419Leu[-]'	No
'DSP(NM_004415)&DSP(NM_001008844)'	chr6	7585921	C>T	16	14	'Ser2809Leu[+]&Ser2210Leu[+]'	No
'DSPP(NM_014208)'	chr4	88537232	A>G	142	2	'Asn1140Asp[+]'	No
'DSPP(NM_014208)'	chr4	88537268	G>A	142	96	'Asp1152Asn[+]'	No
'DSPP(NM_014208)'	chr4	88536899	A>G	154	138	'Asn1029Asp[+]'	No
'DSPP(NM_014208)'	chr4	88536692	A>G	190	174	'Ser960Gly[+]'	No
'DSPP(NM_014208)'	chr4	88537063	A>C	38	82	'Glu1083Asp[+]'	No
'DTX3L(NM_138287)'	chr3	122287757	T>C	38	36	'Met274Thr[+]'	No
'DYSF(NM_001130980)&DYSF(NM_003494)&DYSF(NN	chr2	71795459	C>T	36	38	'Pro951Leu[+]&Pro934Leu[+]&Pr	No
'EFR3A(NM_015137)[+]'	chr8	132991585	G>A	44	64	'Not Det'	No
'EGFLAM(NM_152403)&EGFLAM(NM_182798)'	chr5	38407060	C>T	136	108	'Thr320Met[+]&Thr86Met[+]'	No
'ENC1(NM_003633)'	chr5	73932199	G>T	36	44	'Leu38Ile[-]'	No
'EOMES(NM_005442)[-]'	chr3	27760143	G>C	90	100	'Not Det'	No
'EPPK1(NM_031308)'	chr8	144940290	C>G	28	240	'Asp2378His[-]'	No
'ETNK2(NM_018208)'	chr1	204120952	G>T	8	8	'Pro10Gln[-]'	No
'EVC(NM_153717)'	chr4	5733236	C>G	36	32	'Pro157Ala[+]'	No
'EVPL(NM_001988)'	chr17	74019453	G>A	58	76	'Arg134Cys[-]'	No
'EXOC8(NM_175876)'	chr1	231472537	C>G	50	58	'Glu319Gln[-]'	No
'EYA1(NM_172060)&EYA1(NM_000503)&EYA1(NM_1	chr8	72184072	C>T	76	98	'Arg263His[-]&Arg296His[-]&Arg	No
'FAM101B(NM_182705)'	chr17	293094	A>G	80	92	'Val46Ala[-]'	No
'FAM186A(NM_001145475)'	chr12	50745783	T>A	102	170	'Gln1611Leu[-]'	No
'FAM193A(NM_003704)'	chr4	2673912	C>A	88	98	'Pro424Gln[+]'	No
'FAM26E(NM_153711)'	chr6	116833053	T>C	54	80	'Leu65Pro[+]'	No

'FAM65A(NM_024519)&FAM65A(NM_001193522)&F	chr16	67572934	A>G	66	56	'Gln100Arg[+]&Gln104Arg[+]&G	No
'FANCI(NM_018193)[+]&FANCI(NM_001113378)[+]'	chr15	89833439	C>A	94	58	'Not Det&Not Det'	No
'FBF1(NM_001080542)'	chr17	73921525	T>A	32	30	'Ser277Cys[-]'	No
'FBN3(NM_032447)[-]'	chr19	8155138	G>T	42	46	'Not Det'	No
'FGF5(NM_004464)'	chr4	81207645	A>G	40	64	'Gln209Arg[+]'	No
'FNIP2(NM_020840)'	chr4	159789403	G>C	66	76	'Gly539Arg[+]'	No
'FOXK1(NM_001037165)'	chr7	4800709	C>G	24	24	'Pro571Ala[+]'	No
'FRG1(NM_004477)'	chr4	190876301	C>A	22	140	'Gln143Lys[+]'	No
'FRG2B(NM_001080998)'	chr10	135440214	G>C	134	226	'His11Gln[-]'	No
'FRG2B(NM_001080998)'	chr10	135440216	G>A	134	228	'His11Tyr[-]'	No
'FRG2C(NM_001124759)'	chr3	75714702	A>G	168	80	'Asn120Ser[+]'	No
'FRG2C(NM_001124759)'	chr3	75713564	T>C	198	182	'Cys12Arg[+]'	No
'FRG2C(NM_001124759)'	chr3	75715124	C>T	88	186	'Pro261Ser[+]'	No
'FRG2C(NM_001124759)'	chr3	75715118	G>A	86	184	'Ala259Thr[+]'	No
'FRG2C(NM_001124759)'	chr3	75714917	G>A	92	294	'Ala192Thr[+]'	No
'FRG2C(NM_001124759)'	chr3	75714929	G>A	92	302	'Ala196Thr[+]'	No
'FRG2C(NM_001124759)'	chr3	75715173	C>T	56	204	'Ala277Val[+]'	No
'FRG2C(NM_001124759)'	chr3	75714950	C>A	80	310	'Leu203Met[+]'	No
'FRG2C(NM_001124759)'	chr3	75715181	G>A	48	200	'Gly280Arg[+]'	No
'FRG2C(NM_001124759)'	chr3	75713669	G>A	58	256	'Ala47Thr[+]'	No
'FRG2C(NM_001124759)'	chr3	75714971	C>A	70	316	'Leu210Met[+]'	No
'FRG2C(NM_001124759)[+]'	chr3	75714674	G>A	62	148	'Not Det'	No
'GART(NM_000819)'	chr21	34897196	C>T	68	86	'Arg393Gln[-]'	No
'GDF15(NM_004864)'	chr19	18497024	G>C	24	34	'Val9Leu[+]'	No
'GGA3(NM_014001)&GGA3(NM_138619)&GGA3(NM	chr17	73236063	G>A	38	30	'Pro431Ser[-]&Pro464Ser[-]&Pro	No
'GGT1(NM_013430)'	chr22	25011062	C>G	20	46	'Thr117Ser[+]'	No
'GOLGA6L6(NM_001145004)'	chr15	20740252	C>A	38	48	'Glu500stop[-]'	No
'GPATCH1(NM_018025)[+]'	chr19	33602625	C>T	56	64	'Not Det'	No
'GPR180(NM_180989)'	chr13	95275394	A>G	54	88	'Asp309Gly[+]'	No
'GPR35(NM_001195381)&GPR35(NM_005301)'	chr2	241569454	G>A	26	18	'Val60Ile[+]&Val29Ile[+]'	No

'GRIP2(NM_001080423)'	chr3	14555864	C>T	12	18	'Ala-567Thr[-]'	No
'GXYLT1(NM_173601)&GXYLT1(NM_001099650)'	chr12	42512910	T>A	50	108	'Arg126Ser[-]&Arg95Ser[-]'	No
'GXYLT1(NM_173601)&GXYLT1(NM_001099650)'	chr12	42512924	C>T	44	112	'Ala122Thr[-]&Ala91Thr[-]'	No
'GXYLT1(NM_173601)&GXYLT1(NM_001099650)'	chr12	42512938	T>A	34	110	'His117Leu[-]&His86Leu[-]'	No
'HAUS6(NM_017645)'	chr9	19058483	C>A	22	20	'Ser761Ile[-]'	No
'HAVCR1(NM_012206)'	chr5	156479571	C>T	10	74	'Met158Ile[-]'	No
'HCN4(NM_005477)'	chr15	73615786	G>C	12	18	'Pro883Arg[-]'	No
'HIC2(NM_015094)'	chr22	21800481	G>C	12	10	'Glu433Gln[+]'	No
'HIST1H4G(NM_003547)'	chr6	26247144	T>A	58	10	'Lys21Met[-]'	No
'HLA-A(NM_002116)'	chr6	29911925	C>T	20	42	'His216Tyr[+]'	No
'HLA-DRB1(NM_002124)'	chr6	32548573	C>T	44	116	'Gly238Asp[-]'	No
'HPR(NM_020995)'	chr16	72110948	C>G	84	0	'His339Asp[+]'	No
'HPR(NM_020995)'	chr16	72110637	C>A	66	62	'Thr235Asn[+]'	No
'HSBP1L1(NM_001136180)'	chr18	77726658	C>G	96	74	'Thr33Arg[+]'	No
'HYDIN(NM_032821)'	chr16	70942261	C>A	58	186	'Gly2763Trp[-]'	No
'IGF2BP3(NM_006547)'	chr7	23353246	A>C	28	150	'Ile474Met[-]'	No
'IGFALS(NM_001146006)&IGFALS(NM_004970)'	chr16	1841271	C>T	28	12	'Arg421Gln[-]&Arg383Gln[-]'	No
'IGFN1(NM_001164586)'	chr1	201178904	A>G	34	206	'Glu1628Gly[+]'	No
'IGLL1(NM_020070)'	chr22	23915620	C>T	96	106	'Gly159Ser[-]'	No
'IGLL1(NM_020070)'	chr22	23915631	G>A	98	110	'Pro155Leu[-]'	No
'IGSF22(NM_173588)'	chr11	18741319	C>T	48	92	'Asp214Asn[-]'	No
'IKBKE(NM_014002)[+]&IKBKE(NM_001193322)[+]&I'	chr1	206650186	G>A	40	44	'Not Det&Not Det&Not Det'	No
'IL31(NM_001014336)'	chr12	122657198	G>T	136	144	'Pro86Thr[-]'	No
'ITGA11(NM_001004439)[-]	chr15	68642947	T>C	58	84	'Not Det'	No
'ITPRIPL2(NM_001034841)'	chr16	19126331	C>T	14	4	'Pro183Leu[+]'	No
'KATNAL1(NM_001014380)'	chr13	30854289	A>C	58	64	'Ile78Met[-]'	No
'KCNJ12(NM_021012)'	chr17	21319682	C>T	48	148	'Ser343Leu[+]'	No
'KCTD16(NM_020768)'	chr5	143587022	G>A	54	56	'Ala249Thr[+]'	No
'KIAA0408(NM_014702)'	chr6	127767954	G>A	88	100	'Pro504Ser[-]'	No
'KIAA1244(NM_020340)'	chr6	138628503	G>A	72	90	'Met1314Ile[+]'	No

'KIAA1267(NM_001193466)'	chr17	44144993	C>G	122	0	'Arg525Pro[-]'	No
'KIAA1274(NM_014431)'	chr10	72289648	C>T	44	44	'Arg98Cys[+]'	No
'KIAA1383(NM_019090)'	chr1	232943812	T>C	36	40	'Phe1015Leu[+]'	No
'KIF18A(NM_031217)'	chr11	28119309	T>G	56	72	'Gln62His[-]'	No
'KIF1A(NM_004321)'	chr2	241706353	C>T	28	30	'Asp546Asn[-]'	No
'KIR3DL1(NM_013289)'	chr19	55329854	G>A	120	144	'Arg52His[+]'	No
'KIR3DL1(NM_013289)'	chr19	55330019	C>T	60	90	'Ser107Leu[+]'	No
'KIR3DL1(NM_013289)'	chr19	55329892	A>G	110	166	'Arg65Gly[+]'	No
'KNTC1(NM_014708)'	chr12	123106455	G>T	92	74	'Val2103Phe[+]'	No
'KRT77(NM_175078)'	chr12	53097125	G>A	94	140	'Pro32Ser[-]'	No
'KRTAP10-2(NM_198693)'	chr21	45970920	C>T	132	122	'Arg141His[-]'	No
'KRTAP10-9(NM_198690)'	chr21	46047779	G>A	92	108	'Val231Met[+]'	No
'LGALS16(NM_001190441)'	chr19	40149102	A>G	36	42	'Asn32Ser[+]'	No
'LMAN2(NM_006816)'	chr5	176759170	C>T	16	6	'Ala330Thr[-]'	No
'LOC100132247(NM_001135865)'	chr16	22545897	G>T	72	24	'Lys531Asn[+]'	No
'LOC100132288(NM_001033515)'	chr21	9909078	G>A	66	240	'Ala86Val[-]'	No
'LOC649330(NM_001146181)'	chr1	12907284	T>C	88	162	'Thr287Ala[-]'	No
'LOC649330(NM_001146181)'	chr1	12907285	G>C	74	178	'Ser286Arg[-]'	No
'LPIN2(NM_014646)'	chr18	2951225	C>T	82	76	'Val140Ile[-]'	No
'LPP(NM_005578)'	chr3	188327367	C>T	52	50	'Pro283Leu[+]'	No
'LRRC20(NM_018239)&LRRC20(NM_207119)'	chr10	72083628	C>T	18	6	'Glu81Lys[-]&Glu131Lys[-]'	No
'LRRC40(NM_017768)'	chr1	70644596	G>A	68	44	'Leu248Phe[-]'	No
'LRRC45(NM_144999)'	chr17	79984840	G>A	46	24	'Val243Ile[+]'	No
'LRRC48(NM_001130091)'	chr17	17887186	A>G	100	90	'Lys69Glu[+]'	No
'LRRC50(NM_178452)'	chr16	84203737	G>A	76	54	'Asp435Asn[+]'	No
'LSG1(NM_018385)'	chr3	194365360	C>T	84	112	'Gly580Asp[-]'	No
'LYZL2(NM_183058)'	chr10	30918549	G>C	24	124	'Ala29Gly[-]'	No
'MADD(NM_130470)&MADD(NM_130472)'	chr11	47308065	C>G	70	88	'Thr878Arg[+]&Thr835Arg[+]'	No
'MAN2A2(NM_006122)'	chr15	91452594	C>T	62	58	'Gln412stop[+]'	No
'MASP2(NM_006610)'	chr1	11102940	G>A	76	110	'Thr294Met[-]'	No

'ME1(NM_002395)'	chr6	84108200	T>A	42	36	'Glu83Val[-]'	No
'MED13(NM_005121)'	chr17	60042388	G>A	84	48	'Pro1608Leu[-]'	No
'MEF2A(NM_005587)'	chr15	100211780	A>G	20	140	'Tyr105Cys[+]'	No
'MEF2A(NM_005587)'	chr15	100211761	C>T	18	154	'Pro99Ser[+]'	No
'METRNL(NM_001004431)'	chr17	81052130	A>G	48	32	'His249Arg[+]'	No
'METTL8(NM_024770)'	chr2	172182377	C>T	38	48	'Gly336Asp[-]'	No
'MGEA5(NM_012215)[-]'	chr10	103560160	G>A	76	68	'Not Det'	No
'MICALL2(NM_182924)'	chr7	1488265	G>A	10	8	'Arg109Cys[-]'	No
'MKLN1(NM_001145354)[+]&MKLN1(NM_013255)[+]	chr7	131163376	A>T	8	56	'Not Det&Not Det'	No
'MLL2(NM_003482)'	chr12	49418717	C>T	26	36	'Arg5266His[-]'	No
'MLL3(NM_170606)'	chr7	151945007	C>T	48	92	'Gly838Ser[-]'	No
'MLL3(NM_170606)'	chr7	151882672	C>A	52	166	'Ala1685Ser[-]'	No
'MRPL9(NM_031420)'	chr1	151733293	G>A	56	54	'Thr224Met[-]'	No
'MRPS10(NM_018141)'	chr6	42185567	G>T	18	18	'Phe7Leu[-]'	No
'MUC12(NM_001164462)'	chr7	100645825	C>A	104	228	'Thr3994Lys[+]'	No
'MUC16(NM_024690)'	chr19	9003357	T>C	144	192	'Met13360Val[-]'	No
'MUC16(NM_024690)'	chr19	9002519	G>C	54	170	'His13433Asp[-]'	No
'MUC17(NM_001040105)'	chr7	100679318	A>C	76	218	'Thr1541Pro[+]'	No
'MUC17(NM_001040105)'	chr7	100679316	T>A	72	218	'Val1540Asp[+]'	No
'MUC17(NM_001040105)'	chr7	100677279	G>C	84	274	'Ser861Thr[+]'	No
'MUC2(NM_002457)'	chr11	1092715	G>A	196	124	'Ala1512Thr[+]'	No
'MUC2(NM_002457)'	chr11	1093430	C>A	114	230	'Thr1750Asn[+]'	No
'MUC2(NM_002457)'	chr11	1093094	T>G	42	250	'Val1638Gly[+]'	No
'MUC2(NM_002457)'	chr11	1093393	G>A	28	346	'Gly1738Ser[+]'	No
'MUC2(NM_002457)'	chr11	1092860	C>T	18	312	'Thr1560Met[+]'	No
'MUC21(NM_001010909)'	chr6	30954523	A>G	42	148	'Arg191Gly[+]'	No
'MUC21(NM_001010909)'	chr6	30954347	C>T	12	134	'Ala132Val[+]'	No
'MUC4(NM_018406)'	chr3	195512107	T>A	400	0	'Asp2115Val[-]'	No
'MUC4(NM_018406)'	chr3	195512004	T>G	146	0	'Glu2149Asp[-]'	No
'MUC4(NM_018406)'	chr3	195512186	T>C	252	6	'Ile2089Val[-]'	No

'MUC4(NM_018406)'	chr3	195510217	A>G	162	14	'Val2745Ala[-]'	No
'MUC4(NM_018406)'	chr3	195506473	A>G	60	54	'Val3993Ala[-]'	No
'MUC4(NM_018406)'	chr3	195510194	G>C	110	100	'Leu2753Val[-]'	No
'MUC4(NM_018406)'	chr3	195507226	A>G	164	186	'Val3742Ala[-]'	No
'MUC4(NM_018406)'	chr3	195507062	C>T	56	78	'Asp3797Asn[-]'	No
'MUC4(NM_018406)'	chr3	195506267	C>T	56	82	'Ala4062Thr[-]'	No
'MUC4(NM_018406)'	chr3	195506281	A>G	38	56	'Leu4057Ser[-]'	No
'MUC4(NM_018406)'	chr3	195507107	C>T	112	180	'Ala3782Thr[-]'	No
'MUC4(NM_018406)'	chr3	195506282	A>C	34	56	'Leu4057Val[-]'	No
'MUC4(NM_018406)'	chr3	195509212	G>A	84	210	'Ser3080Leu[-]'	No
'MUC4(NM_018406)'	chr3	195506245	C>A	56	144	'Ser4069Ile[-]'	No
'MUC4(NM_018406)'	chr3	195512302	G>A	66	182	'Pro2050Leu[-]'	No
'MUC4(NM_018406)'	chr3	195509974	A>G	88	272	'Phe2826Ser[-]'	No
'MUC4(NM_018406)'	chr3	195507228	G>C	78	270	'His3741Gln[-]'	No
'MUC4(NM_018406)'	chr3	195508108	G>A	54	276	'Ser3448Leu[-]'	No
'MUC4(NM_018406)'	chr3	195508500	G>C	44	232	'Asp3317Glu[-]'	No
'MUC4(NM_018406)'	chr3	195507262	T>G	48	316	'His3730Pro[-]'	No
'MUC4(NM_018406)'	chr3	195511273	G>A	40	278	'Ala2393Val[-]'	No
'MUC4(NM_018406)'	chr3	195509879	A>G	36	336	'Ser2858Pro[-]'	No
'MUC5B(NM_002458)'	chr11	1267010	A>G	50	76	'Asn2967Ser[+]'	No
'MUC5B(NM_002458)'	chr11	1263932	C>G	116	194	'Thr1941Ser[+]'	No
'MUC5B(NM_002458)'	chr11	1270427	G>A	82	168	'Arg4106His[+]'	No
'MUC5B(NM_002458)'	chr11	1264022	C>T	96	208	'Thr1971Ile[+]'	No
'MUC5B(NM_002458)'	chr11	1269770	C>T	90	224	'Pro3887Leu[+]'	No
'MUC5B(NM_002458)'	chr11	1270361	C>T	66	212	'Thr4084Met[+]'	No
'MUC5B(NM_002458)'	chr11	1267631	C>T	58	214	'Thr3174Met[+]'	No
'MUC5B(NM_002458)'	chr11	1270322	C>G	48	180	'Pro4071Arg[+]'	No
'MUC5B(NM_002458)'	chr11	1265951	C>T	62	328	'Thr2614Met[+]'	No
'MUC5B(NM_002458)'	chr11	1269758	C>T	26	280	'Thr3883Met[+]'	No
'MUC5B(NM_002458)'	chr11	1270408	G>C	14	292	'Ala4100Pro[+]'	No

'MUC6(NM_005961)'	chr11	1017069	G>A	92	312	'Thr1911Met[-]'	No
'MUC6(NM_005961)'	chr11	1017655	G>A	68	252	'Pro1716Ser[-]'	No
'MUC6(NM_005961)'	chr11	1016919	C>T	84	320	'Arg1961Lys[-]'	No
'MYH7B(NM_020884)'	chr20	33574773	A>G	42	40	'Glu372Gly[+]'	No
'MYO18A(NM_078471)'	chr17	27424848	G>A	70	48	'Arg1354Trp[-]'	No
'MYO1E(NM_004998)[-]'	chr15	59430572	G>A	36	32	Not Det'	No
'MYO5B(NM_001080467)'	chr18	47566678	C>G	86	78	'Glu49Gln[-]'	No
'MYT1L(NM_015025)[-]'	chr2	1947113	A>T	64	52	Not Det'	No
'N4BP1(NM_153029)'	chr16	48577065	C>T	44	58	'Arg814Gln[-]'	No
'NACAD(NM_001146334)'	chr7	45123943	A>T	20	52	'Asp612Glu[-]'	No
'NAGLU(NM_000263)'	chr17	40695813	G>A	30	8	'Val597Ile[+]'	No
'NAIF1(NM_197956)'	chr9	130829254	C>T	8	10	'Ala43Thr[-]'	No
'NALCN(NM_052867)[-]'	chr13	101755515	T>A	70	74	Not Det'	No
'NAV2(NM_001111018)&NAV2(NM_145117)'	chr11	19955322	C>T	110	98	'Thr447Met[+]&Thr511Met[+]'	No
'NBPF1(NM_017940)[-]'	chr1	16893854	A>C	14	120	Not Det'	No
'NBPF10(NM_001039703)'	chr1	145367800	G>A	8	4	'Asp3466Asn[+]'	No
'NBPF10(NM_001039703)'	chr1	145323656	A>T	12	110	'Ile1165Phe[+]'	No
'NBPF10(NM_001039703)'	chr1	145323667	C>G	8	116	'Asp1168Glu[+]'	No
'NBPF14(NM_015383)'	chr1	148004783	C>A	120	108	'Ser844Ile[-]'	No
'NCK2(NM_003581)'	chr2	106509501	G>A	44	44	'Val338Met[+]'	No
'NCL(NM_005381)'	chr2	232325414	T>A	44	290	'Glu259Asp[-]'	No
'NCL(NM_005381)'	chr2	232325408	A>C	36	290	'Asp261Glu[-]'	No
'NCOR1(NM_001190440)&NCOR1(NM_001190438)'	chr17	16068396	G>A	38	148	'Ser172Leu[-]&Ser63Leu[-]'	No
'NEB(NM_001164507)'	chr2	152520258	C>T	114	84	'Arg1856Gln[-]'	No
'NF1(NM_001128147)'	chr17	29546083	G>A	72	68	'Val530Ile[+]'	No
'NFX1(NM_147133)'	chr9	33295206	G>A	100	162	'Ala272Thr[+]'	No
'NINL(NM_025176)'	chr20	25443177	T>G	52	70	'Asn1142His[-]'	No
'NOMO1(NM_014287)'	chr16	14988868	A>G	48	110	'Glu1153Gly[+]'	No
'NPHP4(NM_015102)'	chr1	5927943	G>A	38	24	'Ala1110Val[-]'	No
'NPHP4(NM_015102)'	chr1	5965494	C>T	52	44	'Gly605Ser[-]'	No

'NUP210L(NM_207308)'	chr1	154018655	C>T	78	78	'Val1196Ile[-]'	No
'OLFML1(NM_198474)'	chr11	7530844	T>C	50	68	'Ser212Pro[+]'	No
'OR11G2(NM_001005503)'	chr14	20665640	G>A	74	42	'Gly49Asp[+]'	No
'OR11G2(NM_001005503)'	chr14	20665538	C>T	40	42	'Pro15Leu[+]'	No
'OR1D5(NM_014566)'	chr17	2966154	G>A	62	216	'Leu250Phe[-]'	No
'OR2J3(NM_001005216)'	chr6	599209	T>C	70	66	'Leu222Pro[+]'	No
'OR2T11(NM_001001964)'	chr1	248790266	G>C	96	90	'Pro55Arg[-]'	No
'OR2T29(NM_001004694)'	chr1	248722659	C>T	62	0	'Gly39Glu[-]'	No
'OR2T29(NM_001004694)'	chr1	248722671	T>A	82	0	'Lys35Met[-]'	No
'OR2T34(NM_001001821)'	chr1	248737511	A>G	42	94	'Phe183Ser[-]'	No
'OR6B1(NM_001005281)'	chr7	143702008	G>T	32	34	'Ala307Ser[+]'	No
'OSCP1(NM_145047)'	chr1	36898067	T>C	62	68	'Thr131Ala[-]'	No
'OSMR(NM_003999)'	chr5	38921864	G>A	82	118	'Gly578Asp[+]'	No
'P2RX4(NM_002560)[+]'	chr12	121670318	G>A	28	42	Not Det'	No
'PABPC1(NM_002568)'	chr8	101730010	T>C	20	118	'Asp165Gly[-]'	No
'PAICS(NM_006452)&PAICS(NM_001079525)'	chr4	57314612	C>G	52	40	'Ser141Cys[+]&Ser148Cys[+]'	No
'PARD3B(NM_205863)'	chr2	206023483	C>A	60	76	'Thr491Lys[+]'	No
'PBLD(NM_022129)'	chr10	70051910	C>G	68	76	'Leu123Phe[-]'	No
'PCDHA6(NM_031849)'	chr5	140209119	C>G	56	48	'Asp481Glu[+]'	No
'PCDHA9(NM_031857)'	chr5	140229602	G>A	24	46	'Val508Met[+]'	No
'PCDHGA12(NM_032094)'	chr5	140811030	C>T	22	26	'Ala235Val[+]'	No
'PCDHGA4(NM_018917)'	chr5	140734802	G>C	26	30	'Arg12Pro[+]'	No
'PDE3B(NM_000922)'	chr11	14889208	G>A	110	122	'Glu1015Lys[+]'	No
'PDE4DIP(NM_001002811)'	chr1	144930802	T>G	26	92	'Ile303Leu[-]'	No
'PDE4DIP(NM_001198834)&PDE4DIP(NM_001198832)	chr1	144863320	T>C	36	124	'Lys2028Arg[-]&Lys1922Arg[-]'	No
'PDE9A(NM_001001581)&PDE9A(NM_001001585)&P	chr21	44192615	G>A	64	58	'Val518Met[+]&Val378Met[+]&V	No
'PDIA4(NM_004911)'	chr7	148709063	G>C	50	42	'Pro285Arg[-]'	No
'PHF17(NM_199320)'	chr4	129792810	G>A	54	50	'Arg641His[+]'	No
'PHF23(NM_024297)'	chr17	7139747	C>G	32	40	'Val167Leu[-]'	No
'PHTF1(NM_006608)[-]'	chr1	114240881	T>C	54	74	Not Det'	No

'PHYHD1(NM_001100876)&PHYHD1(NM_001100877'	chr9	131700036	C>A	68	76	'Gln146Lys[+]&Gln125Lys[+]'	No
'PIAS4(NM_015897)[+]'	chr19	4029040	C>G	32	30	'Not Det'	No
'PKD2L1(NM_016112)'	chr10	102054823	G>A	92	64	'Arg472Cys[-]'	No
'PLA2G4E(NM_001080490)'	chr15	42281630	C>T	42	32	'Arg540Gln[-]'	No
'PLA2G4F(NM_213600)'	chr15	42437975	C>T	50	54	'Cys554Tyr[-]'	No
'PLCB4(NM_001172646)&PLCB4(NM_182797)'	chr20	9440307	C>T	54	64	'Thr1033Ile[+]&Thr1021Ile[+]'	No
'PLCH1(NM_014996)&PLCH1(NM_001130960)'	chr3	155200133	T>C	72	74	'Met1198Val[-]&Met1236Val[-]'	No
'PLEK(NM_002664)'	chr2	68613681	C>T	78	80	'Arg174Cys[+]'	No
'PLEKHH2(NM_172069)'	chr2	43939505	A>C	74	58	'Lys815Gln[+]'	No
'PML(NM_033250)&PML(NM_033239)'	chr15	74327560	C>G	8	44	'His538Gln[+]&His586Gln[+]'	No
'POTED(NM_174981)'	chr21	15013735	A>G	112	148	'Met535Val[+]'	No
'POTED(NM_174981)'	chr21	14982886	G>A	82	136	'Gly113Ser[+]'	No
'POTED(NM_174981)'	chr21	14982716	T>C	54	180	'Met56Thr[+]'	No
'PRAME(NM_006115)'	chr22	22899234	A>G	58	82	'Trp7Arg[-]'	No
'PRAMEF6(NM_001010889)'	chr1	13001277	G>C	40	152	'Gln136Glu[-]'	No
'PRB4(NM_002723)'	chr12	11461769	G>T	88	214	'Pro50Thr[-]'	No
'PRKCB(NM_002738)'	chr16	24166071	G>A	100	98	'Val378Met[+]'	No
'PRSS1(NM_002769)'	chr7	142460335	A>G	116	158	'Lys170Glu[+]'	No
'PRSS1(NM_002769)'	chr7	142460369	G>A	82	172	'Ser181Asn[+]'	No
'PRSS2(NM_002770)'	chr7	142480002	C>A	136	76	'Ser32Tyr[+]'	No
'PRSS2(NM_002770)'	chr7	142479954	C>T	68	140	'Thr16Ile[+]'	No
'PRSS2(NM_002770)'	chr7	142479912	C>G	64	148	'Ala2Gly[+]'	No
'PRSS2(NM_002770)'	chr7	142479917	C>T	64	158	'Pro4Ser[+]'	No
'PRSS2(NM_002770)[+]'	chr7	142480067	C>T	36	60	'Not Det'	No
'PSG7(NM_002783)'	chr19	43433676	G>C	144	124	'Asn209Lys[-]'	No
'PSMD1(NM_001191037)'	chr2	231934855	G>T	50	52	'Glu209Asp[+]'	No
'PSMD13(NM_175932)'	chr11	244115	G>A	40	0	'Cys57Tyr[+]'	No
'PTH1R(NM_000316)'	chr3	46937272	G>C	56	76	'Gly76Arg[+]'	No
'PUS3(NM_031307)'	chr11	125765995	C>T	128	154	'Arg62Gln[-]'	No
'R3HDM1(NM_015361)'	chr2	136473148	T>C	100	126	'Ile887Thr[+]'	No

'RAB6C(NM_032144)'	chr2	130738163	G>A	58	76	'Ala159Thr[+]' No
'RALGAPA2(NM_020343)'	chr20	20493784	T>C	64	66	'His1410Arg[-]' No
'RANBP2(NM_006267)'	chr2	109380158	C>T	54	62	'Pro1055Ser[+]' No
'RANBP2(NM_006267)'	chr2	109380157	G>T	54	64	'Gln1054His[+]' No
'RANBP2(NM_006267)[+]'	chr2	109367977	A>G	100	132	'Not Det' No
'RASGRP2(NM_001098671)[-]&RASGRP2(NM_001098671)[+]'	chr11	64508558	G>A	34	28	'Not Det&Not Det&Not Det' No
'RBMLX3(NM_001145346)'	chrX	114426193	G>A	72	0	'Arg730Gln[+]' No
'RDH10(NM_172037)'	chr8	74209461	T>G	90	96	'Cys108Gly[+]' No
'RFPL3(NM_006604)&RFPL3(NM_001098535)'	chr22	32756703	C>T	108	144	'Arg251Cys[+]&Arg280Cys[+]' No
'RFPL4B(NM_001013734)'	chr6	112670920	C>A	80	86	'Arg4Ser[+]' No
'RGPD2(NM_001078170)[+]&RGPD1(NM_001024457)[-]'	chr2	87211874	T>C	26	56	'Not Det&Not Det' No
'RNF216(NM_207116)[-]&RNF216(NM_207111)[-]'	chr7	5770454	G>A	16	20	'Not Det&Not Det' No
'RSPH10B(NM_173565)'	chr7	5983063	C>T	10	2	'Met550Ile[-]' No
'RYR1(NM_001042723)'	chr19	38946109	A>G	92	144	'Asn532Ser[+]' No
'SAA1(NM_199161)[+]&SAA1(NM_000331)[+]&SAA1(NM_000331)[-]'	chr11	18290737	T>G	54	0	'Not Det&Not Det&Not Det' No
'SAMD4A(NM_001161577)'	chr14	55251159	C>T	86	94	'Gln307stop[+]' No
'SCLT1(NM_144643)'	chr4	129891542	C>A	54	74	'Met256Ile[-]' No
'SCN4A(NM_000334)'	chr17	62018241	C>T	26	36	'Ala1801Thr[-]' No
'SCTR(NM_002980)'	chr2	120231031	G>A	46	52	'Arg135Trp[-]' No
'SDK1(NM_152744)'	chr7	4260877	C>T	22	28	'Pro1903Leu[+]' No
'SEC14L1(NM_001143998)&SEC14L1(NM_001144001)[-]'	chr17	75208179	C>T	48	38	'Pro587Ser[+]&Pro553Ser[+]' No
'SEC22B(NM_004892)'	chr1	145115783	G>A	34	250	'Arg181His[+]' No
'SEC31B(NM_015490)'	chr10	102247813	A>G	64	70	'Tyr1111His[-]' No
'SEMG1(NM_003007)'	chr20	43836281	G>C	80	118	'Asp115His[+]' No
'SEPT14(NM_207366)'	chr7	55902230	T>C	58	68	'Asp203Gly[-]' No
'SETD8(NM_020382)'	chr12	123875223	C>T	24	242	'Pro60Leu[+]' No
'SH2D3A(NM_005490)'	chr19	6754939	C>T	46	50	'Arg295Gln[-]' No
'SH2D4B(NM_207372)'	chr10	82298130	C>G	28	30	'Leu15Val[+]' No
'SIPA1L2(NM_020808)'	chr1	232561520	G>A	72	46	'Ser1482Leu[-]' No
'SLC16A8(NM_013356)'	chr22	38477014	C>T	8	2	'Gly344Asp[-]' No

'SLC18A1(NM_001142324)'	chr8	20036674	A>G	68	80	'Met149Thr[-]'	No
'SLC35D3(NM_001008783)'	chr6	137245534	G>C	48	56	'Gln317His[+]'	No
'SLC37A1(NM_018964)'	chr21	43982272	A>C	116	90	'Asn356His[+]'	No
'SLC46A3(NM_001135919)'	chr13	29287552	C>T	56	38	'Val109Ile[-]'	No
'SLC50A1(NM_001122839)'	chr1	155109419	C>T	48	52	'Pro92Ser[+]'	No
'SLC5A11(NM_052944)'	chr16	24887017	C>T	62	96	'Leu148Phe[+]'	No
'SLC7A11(NM_014331)'	chr4	139106315	A>G	60	48	'Ile292Thr[-]'	No
'SMC5(NM_015110)'	chr9	72897495	A>G	50	50	'Glu326Gly[+]'	No
'SMCR8(NM_144775)'	chr17	18220213	T>G	116	86	'Phe370Leu[+]'	No
'SOX7(NM_031439)'	chr8	10583616	C>T	66	46	'Gly267Ser[-]'	No
'SPANXC(NM_022661)'	chrX	140335742	G>C	58	178	'Leu68Val[-]'	No
'SPEG(NM_005876)'	chr2	220352921	C>T	50	50	'Pro2583Ser[+]'	No
'SPPL2B(NM_152988)'	chr19	2352990	C>T	16	20	'Arg521Cys[+]'	No
'SPRYD5(NM_032681)'	chr11	55653617	A>C	64	78	'Met144Leu[+]'	No
'SSPO(NM_198455)'	chr7	149474770	G>A	14	12	'Arg190His[+]'	No
'STARD9(NM_020759)'	chr15	42974713	C>T	48	46	'Thr826Met[+]'	No
'STRN3(NM_001083893)'	chr14	31416312	C>G	66	88	'Gly234Arg[-]'	No
'STXBP5(NM_001127715)'	chr6	147636753	A>G	70	88	'Tyr502Cys[+]'	No
'SUSD2(NM_019601)'	chr22	24579157	G>T	26	88	'Gly70Val[+]'	No
'SYNE1(NM_033071)&SYNE1(NM_182961)'	chr6	152665261	C>A	76	0	'Glu3989Asp[-]&Glu4060Asp[-]'	No
'SYNE1(NM_033071)&SYNE1(NM_182961)'	chr6	152686090	G>T	56	78	'Ser3353Tyr[-]&Ser3346Tyr[-]'	No
'SYNE1(NM_033071)&SYNE1(NM_182961)&SYNE1(NM_182961)'	chr6	152631869	C>T	78	54	'Arg5546Gln[-]&Arg5617Gln[-]&Arg5617Gln[-]'	No
'TACC2(NM_206862)'	chr10	123809983	G>T	8	92	'Ala22Ser[+]'	No
'TAGLN2(NM_003564)'	chr1	159888714	G>T	30	50	'Pro159His[-]'	No
'TBC1D16(NM_019020)'	chr17	77984175	G>A	34	38	'Ser188Leu[-]'	No
'TBCD(NM_005993)'	chr17	80885156	A>G	54	74	'Met856Val[+]'	No
'TDRD10(NM_001098475)'	chr1	154516944	C>T	26	28	'Arg250Cys[+]'	No
'TELO2(NM_016111)[+]'	chr16	1550707	G>A	12	26	Not Det'	No
'TENC1(NM_198316)&TENC1(NM_015319)&TENC1(NM_015319)'	chr12	53456223	G>A	78	62	'Arg1120His[+]&Arg1254His[+]&Arg1254His[+]'	No
'TGM3(NM_003245)'	chr20	2290333	C>A	98	0	'Thr13Lys[+]'	No

'TIFA(NM_052864)'	chr4	113199410	T>C	48	50	'Ile55Val[-]'	No
'TLL2(NM_012465)'	chr10	98145865	C>T	72	88	'Ala654Thr[-]'	No
'TMCO4(NM_181719)'	chr1	20082209	G>A	76	84	'Leu145Phe[-]'	No
'TMEM106B(NM_001134232)'	chr7	12263971	G>A	104	100	'Ser134Asn[+]'	No
'TMEM143(NM_018273)'	chr19	48845855	C>T	20	24	'Asp303Asn[-]'	No
'TMEM195(NM_001004320)'	chr7	15240972	T>C	56	74	'Ile426Val[-]'	No
'TMEM229A(NM_001136002)'	chr7	123672082	G>T	52	64	'Leu326Met[-]'	No
'TMPRSS3(NM_024022)'	chr21	43815481	G>A	88	86	'Arg16stop[-]'	No
'TNXB(NM_032470)'	chr6	31977391	C>T	52	0	'Arg-170His[-]'	No
'TOP2B(NM_001068)'	chr3	25705758	C>T	8	2	'Ala11Thr[-]'	No
'TOP3A(NM_004618)'	chr17	18181285	T>C	30	24	'Asn844Ser[-]'	No
'TPRX1(NM_198479)'	chr19	48305586	G>A	82	130	'Pro228Ser[-]'	No
'TPRX1(NM_198479)'	chr19	48305555	G>A	24	146	'Pro238Leu[-]'	No
'TPSAB1(NM_003294)'	chr16	1291622	A>G	26	58	'Thr141Ala[+]'	No
'TPSG1(NM_012467)'	chr16	1272275	C>T	10	4	'Arg193His[-]'	No
'TRHDE(NM_013381)[+]'	chr12	73015416	A>G	40	30	Not Det'	No
'TRIM5(NM_033092)'	chr11	5700399	C>G	58	46	'Val140Leu[-]'	No
'TRIM67(NM_001004342)'	chr1	231344908	A>G	86	94	'Met679Val[+]'	No
'TRRAP(NM_003496)'	chr7	98547145	C>T	22	40	'Arg1607Cys[+]'	No
'TSEN54(NM_207346)'	chr17	73519758	C>G	56	48	'Ser443Cys[+]'	No
'TTN(NM_133432)&TTN(NM_003319)&TTN(NM_133432)'	chr2	179404402	T>C	94	66	'Asn23857Ser[-]&Asn23732Ser[-]'	No
'TUBA3D(NM_080386)'	chr2	132236886	G>A	76	112	'Val78Met[+]'	No
'TYRO3(NM_006293)[+]'	chr15	41853733	A>T	8	46	Not Det'	No
'TYRO3(NM_006293)[+]'	chr15	41862801	G>T	18	112	Not Det'	No
'TYW1B(NM_001145441)&TYW1B(NM_001145440)'	chr7	72193854	G>T	82	92	'Asp-258Glu[-]&Asp-293Glu[-]'	No
'UBXN11(NM_001077262)&UBXN11(NM_145345)&U'	chr1	26608885	C>T	8	28	'Gly370Ser[-]&Gly457Ser[-]&Gly457Ser[-]'	No
'UQCR10(NM_001003684)'	chr22	30163571	G>A	42	26	'Ala62Thr[+]'	No
'USP17L2(NM_201402)'	chr8	11995248	G>A	34	76	'Ala341Val[-]'	No
'VCX(NM_013452)'	chrX	7811810	G>C	8	0	'Ser125Thr[+]'	No
'WDR59(NM_030581)[-]'	chr16	74942798	T>G	26	26	Not Det'	No

'WDR93(NM_020212)'	chr15	90276412	C>A	62	72	'Ser502Arg[+]' No
'ZC3H13(NM_015070)'	chr13	46538138	A>C	92	48	'Met1505Arg[-]' No
'ZMZ1(NM_020338)'	chr10	81070780	A>T	48	46	'Ser979Cys[+]' No
'ZNF141(NM_003441)'	chr4	367169	G>A	12	74	'Glu315Lys[+]' No
'ZNF142(NM_001105537)'	chr2	219513675	C>T	36	26	'Arg319His[-]' No
'ZNF208(NM_007153)'	chr19	22155725	C>G	28	74	'Trp704Ser[-]' No
'ZNF208(NM_007153)'	chr19	22155783	C>T	22	74	'Val685Ile[-]' No
'ZNF208(NM_007153)'	chr19	22155696	T>C	14	60	'Ile714Val[-]' No
'ZNF366(NM_152625)'	chr5	71756519	C>A	48	58	'Val269Phe[-]' No
'ZNF528(NM_032423)'	chr19	52919199	G>A	74	72	'Arg365His[+]' No
'ZNF599(NM_001007248)'	chr19	35250996	C>T	96	86	'Arg237His[-]' No
'ZNF717(NM_001128223)'	chr3	75790513	T>C	334	0	'Tyr64Cys[-]' No
'ZNF717(NM_001128223)'	chr3	75788010	A>C	336	0	'Val255Gly[-]' No
'ZNF717(NM_001128223)'	chr3	75787726	G>A	216	56	'Arg350Cys[-]' No
'ZNF717(NM_001128223)'	chr3	75788115	G>A	246	88	'Thr220Met[-]' No
'ZNF717(NM_001128223)'	chr3	75788076	A>C	236	86	'Val233Gly[-]' No
'ZNF717(NM_001128223)'	chr3	75788023	C>T	242	94	'Val251Ile[-]' No
'ZNF717(NM_001128223)'	chr3	75788152	T>C	146	88	'Thr208Ala[-]' No
'ZNF717(NM_001128223)'	chr3	75788227	A>G	152	100	'Cys183Arg[-]' No
'ZNF717(NM_001128223)'	chr3	75787927	A>G	178	120	'Tyr283His[-]' No
'ZNF717(NM_001128223)'	chr3	75788199	T>C	170	144	'His192Arg[-]' No
'ZNF717(NM_001128223)'	chr3	75788226	C>A	116	100	'Cys183Phe[-]' No
'ZNF717(NM_001128223)'	chr3	75788281	T>C	122	110	'Met165Val[-]' No
'ZNF717(NM_001128223)'	chr3	75788292	T>A	120	114	'Asp161Val[-]' No
'ZNF717(NM_001128223)'	chr3	75787869	C>T	134	136	'Cys302Tyr[-]' No
'ZNF717(NM_001128223)'	chr3	75787876	G>T	134	138	'Leu300Ile[-]' No
'ZNF717(NM_001128223)'	chr3	75787870	A>G	132	136	'Cys302Arg[-]' No
'ZNF717(NM_001128223)'	chr3	75786080	G>T	78	102	'Asp898Glu[-]' No
'ZNF717(NM_001128223)'	chr3	75788130	C>A	138	196	'Gly215Val[-]' No
'ZNF717(NM_001128223)'	chr3	75786381	T>C	88	132	'Lys798Arg[-]' No

'ZNF717(NM_001128223)'	chr3	75788028	G>C	128	194	'Ser249stop[-]'	No
'ZNF717(NM_001128223)'	chr3	75786132	T>C	154	234	'Gln881Arg[-]'	No
'ZNF717(NM_001128223)'	chr3	75787057	G>A	96	146	'His573Tyr[-]'	No
'ZNF717(NM_001128223)'	chr3	75788434	G>T	92	144	'Gln114Lys[-]'	No
'ZNF717(NM_001128223)'	chr3	75787519	C>A	108	176	'Gly419Trp[-]'	No
'ZNF717(NM_001128223)'	chr3	75787809	T>C	110	182	'Tyr322Cys[-]'	No
'ZNF717(NM_001128223)'	chr3	75786163	C>T	142	244	'Glu871Lys[-]'	No
'ZNF717(NM_001128223)'	chr3	75786225	G>A	126	222	'Thr850Ile[-]'	No
'ZNF717(NM_001128223)'	chr3	75787516	C>G	102	180	'Glu420Gln[-]'	No
'ZNF717(NM_001128223)'	chr3	75790444	G>A	118	214	'Pro87Leu[-]'	No
'ZNF717(NM_001128223)'	chr3	75787159	C>T	92	168	'Glu539Lys[-]'	No
'ZNF717(NM_001128223)'	chr3	75788316	C>T	98	184	'Gly153Glu[-]'	No
'ZNF717(NM_001128223)'	chr3	75787996	C>T	114	220	'Gly260Arg[-]'	No
'ZNF717(NM_001128223)'	chr3	75787897	T>C	100	198	'Ile293Val[-]'	No
'ZNF717(NM_001128223)'	chr3	75787486	C>T	82	164	'Glu430Lys[-]'	No
'ZNF717(NM_001128223)'	chr3	75787186	C>T	68	144	'Ala530Thr[-]'	No
'ZNF717(NM_001128223)'	chr3	75788068	A>C	102	220	'Phe236Val[-]'	No
'ZNF717(NM_001128223)'	chr3	75787962	G>C	100	218	'Thr271Ser[-]'	No
'ZNF717(NM_001128223)'	chr3	75787049	C>A	76	170	'Lys575Asn[-]'	No
'ZNF717(NM_001128223)'	chr3	75786385	C>G	64	154	'Asp797His[-]'	No
'ZNF717(NM_001128223)'	chr3	75786261	C>T	88	222	'Gly838Glu[-]'	No
'ZNF717(NM_001128223)'	chr3	75788366	C>A	84	214	'Leu136Phe[-]'	No
'ZNF717(NM_001128223)'	chr3	75788314	T>C	78	200	'Met154Val[-]'	No
'ZNF717(NM_001128223)'	chr3	75788484	A>G	50	142	'Ile97Thr[-]'	No
'ZNF717(NM_001128223)'	chr3	75786417	T>C	50	156	'Tyr786Cys[-]'	No
'ZNF717(NM_001128223)'	chr3	75787372	A>T	50	164	'Leu468Ile[-]'	No
'ZNF717(NM_001128223)'	chr3	75786211	A>G	82	282	'Ser855Pro[-]'	No
'ZNF717(NM_001128223)'	chr3	75786379	T>C	50	172	'Thr799Ala[-]'	No
'ZNF717(NM_001128223)'	chr3	75788088	C>T	70	252	'Arg229Lys[-]'	No
'ZNF717(NM_001128223)'	chr3	75786278	A>C	58	222	'His832Gln[-]'	No

'ZNF717(NM_001128223)'	chr3	75786252	G>T	60	260	'Pro841His[-]'	No
'ZNF717(NM_001128223)'	chr3	75787801	T>C	54	238	'Ser325Gly[-]'	No
'ZNF717(NM_001128223)'	chr3	75786355	T>A	44	194	'Thr807Ser[-]'	No
'ZNF717(NM_001128223)'	chr3	75786036	A>C	36	216	'Phe913Cys[-]'	No
'ZNF717(NM_001128223)'	chr3	75786073	C>G	44	272	'Glu901Gln[-]'	No
'ZNF717(NM_001128223)'	chr3	75788158	G>C	44	286	'Leu206Val[-]'	No
'ZNF717(NM_001128223)'	chr3	75788432	T>A	32	210	'Gln114His[-]'	No
'ZNF717(NM_001128223)'	chr3	75787620	T>C	44	298	'His385Arg[-]'	No
'ZNF717(NM_001128223)'	chr3	75790516	T>A	36	294	'His63Leu[-]'	No
'ZNF717(NM_001128223)'	chr3	75786993	T>A	34	304	'Asn594Ile[-]'	No
'ZNF717(NM_001128223)'	chr3	75788376	G>C	24	268	'Thr133Arg[-]'	No
'ZNF74(NM_003426)'	chr22	20760410	G>T	52	40	'Gly363Cys[+]'	No
'ZNF76(NM_003427)[+]'	chr6	35258039	C>G	48	42	Not Det'	No
'ZNF799(NM_001080821)'	chr19	12501566	C>T	108	94	'Arg549Gln[-]'	No
'ZNF804B(NM_181646)'	chr7	88965873	T>C	56	68	'Ser1193Pro[+]'	No
'ZNF814(NM_001144989)'	chr19	58385748	G>A	92	148	'Ala337Val[-]'	No
'ZNF83(NM_001105550)&ZNF83(NM_001105553)'	chr19	53116748	T>C	102	58	'Asn357Ser[-]&Asn329Ser[-]'	No
'ZSCAN23(NM_001012455)'	chr6	28403808	G>C	70	88	'Pro79Arg[-]'	No

Table S11: Germline Patient 4

Gene	Position	Mutation	Variant Reads	Total Reads	AA Change	HMGD
'AADACL4(NM_001013630)'	12726169	G>A	99	86	'Arg216Gln[+]'	No
'AAGAB(NM_024666)'	67528778	A>T	58	83	'Met110Lys[-]'	No
'ABCB6(NM_005689)'	220078652	C>T	54	47	'Ala492Thr[-]'	No
'ABCB6(NM_005689)'	220074748	C>T	147	141	'Arg814Gln[-]'	No
'ABCD4(NM_005050)'	74759920	G>A	52	44	'Arg251Cys[-]'	No
'ACAP3(NM_030649)[-]'	1231587	G>A	39	28	Not Det'	No
'ACSBG1(NM_001199377)'	78526747	T>A	79	58	'Ile33Phe[-]'	No
'ACSM4(NM_001080454)'	7463324	G>T	53	48	'Ser201Ile[+]'	No
'ACVRL1(NM_000020)'	52314610	C>T	50	61	'Ala482Val[+]'	No
'ADCY9(NM_001116)'	4165257	C>A	61	77	'Val63Phe[-]'	No
'AFM(NM_001133)'	74347523	T>C	34	32	'Phe11Leu[+]'	No
'AGAP3(NM_031946)'	150840440	A>T	67	80	'Glu762Asp[+]'	No
'AKAP6(NM_004274)'	33292645	C>T	79	75	'Arg1876Cys[+]'	No
'AKAP9(NM_147185)'	91646406	G>A	65	86	'Arg1276Gln[+]'	No
'ALDH8A1(NM_022568)'	135265083	C>T	40	37	'Ala54Thr[-]'	No
'ALG12(NM_024105)'	50303575	G>A	58	58	'Arg211Cys[-]'	No
'ALPPL2(NM_031313)'	233273101	C>G	36	118	'Ala258Gly[+]'	No
'AP3M2(NM_001134296)'	42024759	C>T	113	110	'Thr294Met[+]'	No
'APOB(NM_000384)'	21250902	G>A	89	74	'Ser622Phe[-]'	No
'APOB(NM_000384)'	21238259	C>T	99	102	'Arg1164Lys[-]'	No
'APOBEC4(NM_203454)'	183616866	A>G	64	58	'Phe351Leu[-]'	No
'AQP12B(NM_001102467)'	241621908	G>A	49	51	'Ala116Val[-]'	No
'ARHGAP4(NM_001666)[-]&ARHGAP4(NM_001164)	153173422	G>A	25	34	Not Det&Not Det'	No
'ARHGEF15(NM_173728)'	8218279	G>C	74	79	'Asp349His[+]'	No
'ARHGEF26(NM_015595)'	153840795	A>C	65	73	'Arg338Ser[+]'	No
'ARID5A(NM_212481)[+]'	97216832	C>A	31	32	Not Det'	No
'ARMC4(NM_018076)'	28101542	T>C	54	49	'Met1012Val[-]'	No
'ARMC5(NM_001105247)'	31470886	T>A	13	19	'Phe14Tyr[+]'	No
'ARSD(NM_001669)'	2827939	C>T	27	25	'Arg406Gln[-]'	No
'ARSF(NM_004042)'	3028209	A>C	64	57	'Asn436His[+]'	No

'ARTN(NM_057090)'	44401760	C>T	30	18	'Ala27Val[+]'	No
'ASB11(NM_080873)&ASB11(NM_001012428)'	15307715	A>G	54	70	'Ile189Thr[-]&Ile168Thr[-]'	No
'ASCC2(NM_032204)'	30196980	C>T	98	87	'Ser563Asn[-]'	No
'ASRGL1(NM_001083926)'	62156681	G>A	82	93	'Val190Ile[+]'	No
'ASXL2(NM_018263)'	25991689	T>C	55	75	'Ser185Gly[-]'	No
'ATG2A(NM_015104)'	64668492	G>A	11	8	'Arg1398Trp[-]'	No
'ATN1(NM_001007026)'	7047911	G>A	35	35	'Ala929Thr[+]'	No
'ATP11A(NM_015205)'	113516870	C>G	126	128	'Thr991Ser[+]'	No
'ATP13A5(NM_198505)'	193081122	G>T	52	59	'Ser96Tyr[-]'	No
'ATP8A2(NM_016529)'	26153951	C>T	62	31	'Arg625Trp[+]'	No
'AZI1(NM_001009811)'	79172711	G>A	39	43	'Pro418Leu[-]'	No
'B3GNT9(NM_033309)'	67183533	A>G	36	28	'Tyr286His[-]'	No
'BCL2L10(NM_020396)[-]'	52402177	G>T	83	61	Not Det'	No
'BCLAF1(NM_001077441)'	136600949	G>A	21	113	'Ser19Phe[-]'	No
'BCLAF1(NM_001077441)&BCLAF1(NM_001077440)	136599885	C>A	20	59	'Arg45Met[-]&Arg43Met[-]'	No
'BRD9(NM_001009877)&BRD9(NM_023924)'	878551	A>G	56	54	'Val344Ala[-]&Val397Ala[-]'	No
'BZRAP1(NM_004758)&BZRAP1(NM_024418)'	56386607	G>T	16	104	'Asp1342Glu[-]&Asp1282Glu[-]'	No
'C14orf109(NM_015676)&C14orf109(NM_0010986)	93652787	C>T	222	240	'Thr56Ile[+]&Thr94Ile[+]'	No
'C14orf49(NM_152592)'	95884225	C>A	75	68	'Ala956Ser[-]'	No
'C15orf2(NM_018958)'	24924042	G>A	78	58	'Gly1010Arg[+]'	No
'C15orf39(NM_015492)'	75498486	C>T	51	56	'His33Tyr[+]'	No
'C15orf55(NM_175741)'	34640797	G>A	30	31	'Arg215His[+]'	No
'C18orf34(NM_001105528)&C18orf34(NM_198995)	30795529	G>A	28	29	'Thr688Ile[-]&Thr650Ile[-]'	No
'C19orf40(NM_152266)'	33467575	C>T	59	80	'Thr212Met[+]'	No
'C19orf60(NM_001100419)&C19orf60(NM_001100419)'	18700374	G>A	16	9	'Ala90Thr[+]&Ala112Thr[+]'	No
'C1orf129(NM_001163629)'	170934292	G>A	60	74	'Glu126Lys[+]'	No
'C5orf45(NM_016175)&C5orf45(NM_001017987)'	179267897	G>A	21	21	'Ser171Phe[-]&Ser116Phe[-]'	No
'C8A(NM_000562)'	57373737	G>A	92	157	'Arg444His[+]'	No
'C8orf86(NM_207412)'	38369982	C>G	59	61	'Glu199Gln[-]'	No
'C9orf68(NM_001039395)'	4622472	C>A	57	68	'Glu178Asp[-]'	No
'CAND2(NM_001162499)&CAND2(NM_012298)'	12858380	T>A	22	30	'Leu650Gln[+]&Leu557Gln[+]'	No
'CCBL2(NM_001008661)&CCBL2(NM_001008662)'	89414776	A>T	62	61	'Leu380Gln[-]&Leu346Gln[-]'	No
'CCDC136(NM_022742)'	128444785	C>T	33	38	'Thr251Met[+]'	No

'CCDC61(NM_001080402)'	46506358	G>T	179	171	'Val85Leu[+]'	No
'CCRN4L(NM_012118)'	139964437	A>G	35	64	'Thr134Ala[+]'	No
'CD1B(NM_001764)'	158299666	C>T	37	39	'Gly195Arg[-]'	No
'CD276(NM_001024736)'	73995247	C>T	144	109	'Pro185Ser[+]'	No
'CELA2B(NM_015849)'	15813844	G>T	106	103	'Gly235Val[+]'	No
'CENPBD1(NM_145039)'	90037882	C>T	154	153	'Cys150Tyr[-]'	No
'CEP350(NM_014810)'	180044254	A>G	100	105	'Ile1889Val[+]'	No
'CGNL1(NM_032866)'	57816803	C>T	80	82	'Arg965Cys[+]'	No
'CHERP(NM_006387)'	16652840	T>G	105	101	'Asn14His[-]'	No
'CHRDL1(NM_145234)&CHRDL1(NM_001143982)&	109924833	C>T	96	112	'Gly343Arg[-]&Gly344Arg[-]&'	No
'CILP2(NM_153221)'	19656047	G>T	14	7	'Arg898Leu[+]'	No
'CKMT1B(NM_020990)'	43888677	A>G	150	184	'Lys275Arg[+]'	No
'CLEC18B(NM_001011880)[-]'	74443542	G>C	373	390	Not Det'	No
'CLIC3(NM_004669)'	139889162	C>A	16	15	'Ala228Ser[-]'	No
'CNKSR1(NM_006314)'	26515956	C>A	193	228	'His687Asn[+]'	No
'CNTNAP3(NM_033655)'	39118196	C>A	258	0	'Gly714Val[-]'	No
'COL12A1(NM_004370)[-]&COL12A1(NM_080645)[-]	75823463	G>A	87	103	Not Det&Not Det'	No
'COL20A1(NM_020882)'	61957039	G>A	13	15	'Gly1123Asp[+]'	No
'COL4A1(NM_001845)[-]'	110844637	G>A	67	69	Not Det'	No
'COL4A5(NM_033380)'	107834411	C>A	43	54	'Ala430Asp[+]'	No
'COL6A2(NM_058174)'	47542052	C>T	40	34	'Pro518Ser[+]'	No
'COL6A3(NM_004369)&COL6A3(NM_057167)&COL	238249370	G>T	64	94	'Ala2730Asp[-]&Ala2524Asp[-]'	No
'COL9A3(NM_001853)'	61470065	G>A	54	66	'Ala606Thr[+]'	No
'COX7A2(NM_001865)'	75953470	C>T	60	71	'Cys26Tyr[-]'	No
'CPD(NM_001304)'	28783346	A>T	58	68	'Gln1137Leu[+]'	No
'CPXM2(NM_198148)'	125521563	C>T	56	45	'Trp534stop[-]'	No
'CRB2(NM_173689)'	126125327	G>A	25	33	'Arg93His[+]'	No
'CSPP1(NM_024790)'	68026086	C>T	30	22	'Pro421Ser[+]'	No
'CT45A5(NM_001172288)'	134948078	C>T	219	250	'Gly83Arg[-]'	No
'CTAG2(NM_172377)'	153880514	T>A	193	229	'Gln144His[-]'	No
'CTSL2(NM_001333)'	99800264	A>C	79	85	'Phe21Cys[-]'	No
'CXorf40A(NM_178124)'	148627384	A>G	119	0	'Thr70Ala[+]'	No
'CYP21A2(NM_000500)'	31973653	A>T	76	29	'His63Leu[+]'	No

'CYP4F3(NM_000896)'	15752322	C>T	45	53	'Arg33Cys[+]'	No
'DBF4(NM_006716)[+]'	87506099	A>C	47	46	'Not Det'	No
'DBH(NM_000787)'	136521726	G>A	60	56	'Ala506Thr[+]'	No
'DCP1B(NM_152640)[-]'	2064733	T>C	124	123	'Not Det'	No
'DDX50(NM_024045)'	70670991	C>T	57	46	'Arg210Cys[+]'	No
'DDX60L(NM_001012967)'	169383049	T>G	97	93	'Glu136Ala[-]'	No
'DENND1A(NM_020946)'	126144390	G>T	13	12	'Ala784Asp[-]'	No
'DHRS7C(NM_001105571)'	9676115	C>G	69	81	'Glu232Asp[-]'	No
'DHX58(NM_024119)'	40263807	G>A	68	64	'Ala35Val[-]'	No
'DLGAP1(NM_004746)&DLGAP1(NM_001003809)'	3534205	G>T	110	119	'Asn822Lys[-]&Asn520Lys[-]'	No
'DMPK(NM_001081560)&DMPK(NM_004409)&DM'	46274624	G>A	133	156	'Thr539Met[-]&Thr544Met[-]'	No
'DNAH12(NM_178504)[-]'	57431752	T>A	56	0	'Not Det'	No
'DNAH17(NM_173628)'	76482076	G>A	79	76	'Pro2414Leu[-]'	No
'DNAH3(NM_017539)'	21093012	C>T	74	62	'Glu972Lys[-]'	No
'DNAH7(NM_018897)'	196746520	G>A	76	96	'Thr1987Met[-]'	No
'DNAJC21(NM_001012339)'	34941263	G>A	41	33	'Asp320Asn[+]'	No
'DRG2(NM_001388)'	18003919	G>A	151	128	'Val193Ile[+]'	No
'DSPP(NM_014208)'	88537232	A>G	716	5	'Asn1140Asp[+]'	No
'DSPP(NM_014208)'	88537063	A>C	234	248	'Glu1083Asp[+]'	No
'DUOX2(NM_014080)'	45389453	G>C	116	124	'Ala1277Gly[-]'	No
'DUOX2(NM_014080)'	45390213	C>T	32	38	'Val1187Ile[-]'	No
'DUOX2(NM_014080)[-]'	45391856	G>A	85	131	'Not Det'	No
'EEF2K(NM_013302)'	22277748	G>T	48	64	'Arg493Leu[+]'	No
'EFHC1(NM_018100)&EFHC1(NM_001172420)'	52288943	C>T	41	45	'Ala88Val[+]&Ala69Val[+]'	No
'EGFR(NM_005228)'	55259448	C>T	84	84	'Arg836Cys[+]'	No
'EPB41L5(NM_020909)'	120925549	C>T	90	96	'Pro701Ser[+]'	No
'EPPK1(NM_031308)'	144946391	C>T	17	18	'Arg344Lys[-]'	No
'F10(NM_000504)'	113803311	A>G	49	50	'Lys316Arg[+]'	No
'FAM184B(NM_015688)[-]'	17634256	C>A	11	167	'Not Det'	No
'FAM186A(NM_001145475)'	50745783	T>A	498	193	'Gln1611Leu[-]'	No
'FAM186A(NM_001145475)'	50745858	T>G	300	341	'Glu1586Ala[-]'	No
'FAM186A(NM_001145475)'	50745703	T>G	201	369	'Thr1638Pro[-]'	No
'FAM192A(NM_024946)'	57201066	T>A	84	125	'Ile141Leu[-]'	No

'FAM20C(NM_020223)'	299843	G>A	28	26	'Arg551His[+]'	No
'FAM63A(NM_001163258)&FAM63A(NM_018379)8'	150972959	A>T	50	46	'Tyr285Asn[-]&Tyr237Asn[-]&'	No
'FAM75A6(NM_001145196)'	43626820	G>C	66	11	'Arg623Gly[-]'	No
'FAM86A(NM_201400)&FAM86A(NM_201598)'	5140539	C>T	167	150	'Glu124Lys[-]&Glu90Lys[-]'	No
'FAT1(NM_005245)'	187584530	G>A	74	92	'Ser1168Leu[-]'	No
'FAT4(NM_024582)'	126412106	C>G	115	110	'Ser4710Cys[+]'	No
'FBXW10(NM_031456)'	18671961	C>T	264	0	'Arg607Cys[+]'	No
'FBXW8(NM_012174)&FBXW8(NM_153348)'	117383224	G>A	103	98	'Cys94Tyr[+]&Cys160Tyr[+]'	No
'FCGR2C(NM_201563)'	161559571	C>T	202	0	'Thr118Ile[+]'	No
'FCGR3A(NM_001127593)&FCGR3A(NM_00112759)	161518214	T>C	118	456	'Ile106Val[-]&Ile105Val[-]&Ile'	No
'FFAR3(NM_005304)'	35850022	A>G	72	62	'Asn77Ser[+]'	No
'FLG(NM_002016)'	152279561	C>T	224	237	'Asp2601Asn[-]'	No
'FLG(NM_002016)'	152282684	G>A	326	346	'Arg1560Cys[-]'	No
'FLYWCH2(NM_001142499)'	2946541	G>A	48	47	'Ala31Thr[+]'	No
'FOXD4L1(NM_012184)'	114257319	C>G	54	49	'Asn162Lys[+]'	No
'FPGT-TNNI3K(NM_001112808)&TNNI3K(NM_0159)	74957907	G>C	92	93	'Glu871Gln[+]&Glu770Gln[+]'	No
'FRG2C(NM_001124759)'	75714702	A>G	502	239	'Asn120Ser[+]'	No
'FRG2C(NM_001124759)'	75714337	T>G	598	298	'Ile106Ser[+]'	No
'FRG2C(NM_001124759)'	75714345	G>T	388	612	'Asp109Tyr[+]'	No
'FRG2C(NM_001124759)'	75714917	G>A	270	730	'Ala192Thr[+]'	No
'FRG2C(NM_001124759)'	75714929	G>A	265	727	'Ala196Thr[+]'	No
'FRG2C(NM_001124759)'	75715118	G>A	238	705	'Ala259Thr[+]'	No
'FRG2C(NM_001124759)'	75714950	C>A	251	748	'Leu203Met[+]'	No
'FRG2C(NM_001124759)'	75715124	C>T	238	729	'Pro261Ser[+]'	No
'FRG2C(NM_001124759)'	75713654	G>A	224	776	'Gly42Arg[+]'	No
'FRG2C(NM_001124759)'	75713669	G>A	213	746	'Ala47Thr[+]'	No
'FRG2C(NM_001124759)'	75713618	A>T	201	798	'Thr30Ser[+]'	No
'FRG2C(NM_001124759)'	75714971	C>A	184	816	'Leu210Met[+]'	No
'FRG2C(NM_001124759)'	75715173	C>T	147	704	'Ala277Val[+]'	No
'FRG2C(NM_001124759)'	75715181	G>A	134	677	'Gly280Arg[+]'	No
'FRG2C(NM_001124759)[+]'	75714674	G>A	149	440	'Not Det'	No
'GDF15(NM_004864)'	18497024	G>C	83	0	'Val9Leu[+]'	No
'GGT1(NM_013430)'	25011031	C>T	13	44	'Arg107Cys[+]'	No

'GLT25D1(NM_024656)'	17692146	C>T	117	111	'Arg588Cys[+]'	No
'GOLGA6B(NM_018652)'	72954638	A>G	301	2	'Glu298Gly[+]'	No
'GOLGA6L6(NM_001145004)'	20740252	C>A	166	0	'Glu500stop[-]'	No
'GPAT2(NM_207328)[-]'	96691925	C>G	12	25	Not Det'	No
'GPR63(NM_030784)'	97246485	T>C	149	131	'Ile375Val[-]'	No
'GPT(NM_005309)[+]'	145731881	C>T	8	13	Not Det'	No
'GTF3C4(NM_012204)'	135553706	G>A	70	54	'Gly234Arg[+]'	No
'GXYLT1(NM_173601)'	42523624	T>C	75	66	'Asn84Ser[-]'	No
'HDAC7(NM_001098416)&HDAC7(NM_015401)'	48181902	G>A	271	247	'Pro724Ser[-]&Pro761Ser[-]'	No
'HEY2(NM_012259)'	126080563	G>C	23	21	'Cys210Ser[+]'	No
'HGC6.3(NM_001129895)'	168376869	C>T	155	93	'Gly155Glu[-]'	No
'HGC6.3(NM_001129895)'	168377119	T>C	34	184	'Met72Val[-]'	No
'HIP1R(NM_003959)'	123341637	C>T	11	9	'Arg564Trp[+]'	No
'HIRA(NM_003325)[-]'	19363318	G>A	163	164	Not Det'	No
'HRNR(NM_001009931)'	152187606	G>A	116	884	'Arg2167Cys[-]'	No
'HSD17B1(NM_000413)'	40706596	C>T	29	26	'Ala238Val[+]'	No
'IFNA4(NM_021068)'	21187025	G>C	224	234	'Ala169Gly[-]'	No
'IFNAR1(NM_000629)'	34713474	C>T	72	59	'Arg124Cys[+]'	No
'ILKAP(NM_030768)[-]'	239092386	G>A	29	37	Not Det'	No
'IMPG2(NM_016247)'	100961565	C>T	104	100	'Ala997Thr[-]'	No
'INF2(NM_022489)'	105174808	G>C	36	27	'Asp591His[+]'	No
'INPP4A(NM_001134224)&INPP4A(NM_001134225)	99172172	G>A	238	220	'Ala580Thr[+]&Ala575Thr[+]'	No
'INSC(NM_001031853)&INSC(NM_001042536)'	15197468	C>T	64	75	'Arg127Trp[+]&Arg80Trp[+]'	No
'ITGB2(NM_000211)'	46309353	G>A	21	26	'Ala572Val[-]'	No
'ITPRIP(NM_033397)'	106075482	C>T	23	14	'Gly110Arg[-]'	No
'JMJD7-PLA2G4B(NM_005090)'	42120342	A>G	17	6	'Glu7Gly[+]'	No
'KCNH6(NM_030779)'	61601584	A>G	75	75	'Tyr54Cys[+]'	No
'KIAA0319L(NM_024874)'	35915492	G>A	91	69	'Arg777Trp[-]'	No
'KIAA0467(NM_015284)'	43897496	G>A	82	126	'Arg834His[+]'	No
'KIAA1267(NM_001193466)'	44144993	C>G	126	0	'Arg525Pro[-]'	No
'KIAA1586(NM_020931)'	56918751	C>T	28	35	'Ala485Val[+]'	No
'KIR3DL1(NM_013289)'	55329854	G>A	197	234	'Arg52His[+]'	No
'KRT7(NM_005556)'	52628942	C>T	41	43	'Arg110Trp[+]'	No

'KRT84(NM_033045)'	52777428	C>T	45	35	'Arg234Gln[-]'	No
'KRTAP10-9(NM_198690)'	46047779	G>A	415	0	'Val231Met[+]'	No
'KRTAP5-10(NM_001012710)'	71276769	G>A	40	62	'Val46Ile[+]'	No
'KRTAP9-4(NM_033191)'	39406231	G>T	249	285	'Gly87Trp[+]'	No
'LOC100132247(NM_001135865)'	22545897	G>T	49	110	'Lys531Asn[+]'	No
'LOC100132288(NM_001033515)'	9909078	G>A	297	701	'Ala86Val[-]'	No
'LOC100132288(NM_001033515)'	9909079	C>T	274	725	'Ala86Thr[-]'	No
'LOC100132288(NM_001033515)'	9909204	C>T	186	801	'Arg44His[-]'	No
'LOC100132288(NM_001033515)'	9909217	C>A	158	717	'Ala40Ser[-]'	No
'LOC649330(NM_001146181)'	12907508	T>C	185	438	'Glu212Gly[-]'	No
'LOC649330(NM_001146181)'	12907533	T>C	163	400	'Ile204Val[-]'	No
'LOC649330(NM_001146181)'	12907496	T>C	179	487	'Lys216Arg[-]'	No
'LOC649330(NM_001146181)'	12907848	G>C	78	536	'Arg99Gly[-]'	No
'LST-3TM12(NM_001009562)'	21229413	G>A	96	108	'Gly545Glu[+]'	No
'LST-3TM12(NM_001009562)'	21242894	C>T	46	54	'Leu593Phe[+]'	No
'LTK(NM_001135685)[-]&LTK(NM_002344)[-]&LTK(	41797736	G>A	67	37	Not Det&Not Det&Not Det'	No
'LUZP4(NM_016383)'	114541251	T>C	38	94	'Val275Ala[+]'	No
'LUZP4(NM_016383)'	114541249	A>G	35	93	'Ile274Met[+]'	No
'LYZ(NM_000239)'	69744020	G>A	72	69	'Gly90Glu[+]'	No
'MAGEC1(NM_005462)'	140993947	T>C	101	0	'Ser253Pro[+]'	No
'MAGEC1(NM_005462)'	140993945	T>C	96	0	'Phe252Ser[+]'	No
'MAGEC1(NM_005462)'	140994066	G>C	78	267	'Gln292His[+]'	No
'MAGEC3(NM_138702)&MAGEC3(NM_177456)'	140985243	G>T	110	126	'Val567Phe[+]&Val269Phe[+]'	No
'MAPK6(NM_002748)'	52353498	C>G	72	62	'Leu290Val[+]'	No
'MATN4(NM_030590)&MATN4(NM_003833)'	43929790	G>A	102	89	'His240Tyr[-]&His281Tyr[-]'	No
'MBD5(NM_018328)'	149226318	A>G	62	69	'Asn269Ser[+]'	No
'MEP1B(NM_005925)'	29797927	A>G	107	120	'Asn697Ser[+]'	No
'MIA3(NM_198551)'	222794629	G>A	130	133	'Gly88Arg[+]'	No
'MIA3(NM_198551)'	222800921	C>T	72	85	'Thr120Met[+]'	No
'MIA3(NM_198551)'	222801661	A>T	85	102	'Thr367Ser[+]'	No
'MICAL3(NM_015241)'	18300278	C>T	48	44	'Glu1717Lys[-]'	No
'MICALL2(NM_182924)'	1487278	G>A	16	19	'Ser153Phe[-]'	No
'MLL3(NM_170606)'	151945007	C>T	130	319	'Gly838Ser[-]'	No

'MMP10(NM_002425)'	102643636	C>A	72	76	'Ala390Ser[-]'	No
'MMP15(NM_002428)'	58075704	A>G	57	63	'Tyr365Cys[+]'	No
'MMP19(NM_002429)'	56230980	C>T	113	136	'Arg456Gln[-]'	No
'MPDZ(NM_003829)'	13176248	T>C	96	112	'Ile940Val[-]'	No
'MRPL45(NM_032351)'	36453208	T>C	172	202	'Phe20Ser[+]'	No
'MRPS22(NM_020191)'	139074528	G>A	68	70	'Asp295Asn[+]'	No
'MUC12(NM_001164462)'	100645731	G>A	81	919	'Glu3963Lys[+]'	No
'MUC16(NM_024690)'	8979223	G>C	110	99	'Pro14050Ala[-]'	No
'MUC16(NM_024690)'	9072561	G>A	265	331	'Thr4962Ile[-]'	No
'MUC2(NM_002457)'	1092715	G>A	528	400	'Ala1512Thr[+]'	No
'MUC2(NM_002457)'	1092998	C>T	140	859	'Thr1606Met[+]'	No
'MUC2(NM_002457)'	1093094	T>G	130	869	'Val1638Gly[+]'	No
'MUC2(NM_002457)'	1092973	C>T	114	884	'Pro1598Ser[+]'	No
'MUC2(NM_002457)'	1093324	G>A	85	914	'Gly1715Ser[+]'	No
'MUC2(NM_002457)'	1093298	C>T	44	952	'Thr1706Met[+]'	No
'MUC4(NM_018406)'	195512186	T>C	963	0	'Ile2089Val[-]'	No
'MUC4(NM_018406)'	195512107	T>A	997	0	'Asp2115Val[-]'	No
'MUC4(NM_018406)'	195512004	T>G	1000	0	'Glu2149Asp[-]'	No
'MUC4(NM_018406)'	195510217	A>G	386	4	'Val2745Ala[-]'	No
'MUC4(NM_018406)'	195506473	A>G	219	14	'Val3993Ala[-]'	No
'MUC4(NM_018406)'	195506569	A>G	307	92	'Val3961Ala[-]'	No
'MUC4(NM_018406)'	195506281	A>G	175	99	'Leu4057Ser[-]'	No
'MUC4(NM_018406)'	195506282	A>C	162	97	'Leu4057Val[-]'	No
'MUC4(NM_018406)'	195508796	C>G	121	85	'Val3219Leu[-]'	No
'MUC4(NM_018406)'	195507226	A>G	552	431	'Val3742Ala[-]'	No
'MUC4(NM_018406)'	195510707	T>G	348	542	'Thr2582Pro[-]'	No
'MUC4(NM_018406)'	195509212	G>A	315	657	'Ser3080Leu[-]'	No
'MUC4(NM_018406)'	195509974	A>G	269	718	'Phe2826Ser[-]'	No
'MUC4(NM_018406)'	195507107	C>T	209	756	'Ala3782Thr[-]'	No
'MUC4(NM_018406)'	195507262	T>G	200	798	'His3730Pro[-]'	No
'MUC4(NM_018406)'	195506746	G>A	53	215	'Ala3902Val[-]'	No
'MUC4(NM_018406)'	195515017	A>G	157	750	'Val1145Ala[-]'	No
'MUC4(NM_018406)'	195507251	G>T	166	834	'Pro3734Thr[-]'	No

'MUC4(NM_018406)'	195507228	G>C	146	853	'His3741Gln[-]'	No
'MUC4(NM_018406)'	195511076	T>A	144	854	'Thr2459Ser[-]'	No
'MUC5B(NM_002458)'	1264742	G>C	266	1	'Arg2211Pro[+]'	No
'MUC5B(NM_002458)'	1269398	C>T	259	66	'Thr3763Ile[+]'	No
'MUC5B(NM_002458)'	1267291	T>C	589	411	'Ser3061Pro[+]'	No
'MUC5B(NM_002458)'	1267289	A>C	539	450	'Lys3060Thr[+]'	No
'MUC5B(NM_002458)'	1269770	C>T	445	555	'Pro3887Leu[+]'	No
'MUC5B(NM_002458)'	1263932	C>G	435	565	'Thr1941Ser[+]'	No
'MUC5B(NM_002458)'	1267010	A>G	268	362	'Asn2967Ser[+]'	No
'MUC5B(NM_002458)'	1270361	C>T	217	645	'Thr4084Met[+]'	No
'MUC5B(NM_002458)'	1265906	C>T	251	748	'Thr2599Ile[+]'	No
'MUC5B(NM_002458)'	1270427	G>A	204	621	'Arg4106His[+]'	No
'MUC5B(NM_002458)'	1265951	C>T	197	799	'Thr2614Met[+]'	No
'MUC5B(NM_002458)'	1267631	C>T	180	742	'Thr3174Met[+]'	No
'MUC5B(NM_002458)'	1269965	C>A	148	799	'Thr3952Asn[+]'	No
'MUC5B(NM_002458)'	1269758	C>T	136	862	'Thr3883Met[+]'	No
'MUC5B(NM_002458)'	1265998	C>A	96	903	'Leu2630Ile[+]'	No
'MUC5B(NM_002458)[+]'	1252648	G>A	37	55	Not Det'	No
'MUC6(NM_005961)'	1017069	G>A	193	806	'Thr1911Met[-]'	No
'MUC6(NM_005961)'	1016733	G>T	146	827	'Thr2023Lys[-]'	No
'MUC6(NM_005961)'	1016919	C>T	128	872	'Arg1961Lys[-]'	No
'MYBPC2(NM_004533)'	50946779	C>T	67	60	'Arg311stop[+]'	No
'MYBPHL(NM_001010985)'	109839482	C>T	215	202	'Arg218His[-]'	No
'NACAD(NM_001146334)'	45123943	A>T	27	46	'Asp612Glu[-]'	No
'NASP(NM_001195193)&NASP(NM_002482)'	46073586	G>A	59	68	'Gly271Ser[+]&Gly335Ser[+]'	No
'NAV2(NM_001111018)&NAV2(NM_145117)&NAV2(NM_145117)'	20065789	C>T	38	36	'Pro993Leu[+]&Pro1057Leu[+]'	No
'NBPF10(NM_001039703)'	145323656	A>T	11	86	'Ile1165Phe[+]'	No
'NCKAP5(NM_207363)'	133887681	A>T	63	63	'His70Gln[-]'	No
'NECAP2(NM_001145277)&NECAP2(NM_001145277)'	16778370	G>A	39	43	'Arg176Gln[+]&Arg150Gln[+]'	No
'NES(NM_006617)'	156640469	C>T	37	24	'Gly1171Ser[-]'	No
'NFATC2(NM_001136021)&NFATC2(NM_012340)'	50140058	G>A	49	36	'Pro221Leu[-]&Pro241Leu[-]'	No
'NGEF(NM_019850)&NGEF(NM_001114090)'	233756151	C>T	65	60	'Asp397Asn[-]&Asp305Asn[-]'	No
'NIN(NM_020921)'	51224794	G>C	70	81	'Ser985Cys[-]'	No

'NKTR(NM_005385)'	42679486	A>G	71	80	'Lys764Glu[+]'	No
'NLRP5(NM_153447)'	56539142	G>A	63	59	'Val515Met[+]'	No
'NMNAT2(NM_015039)&NMNAT2(NM_170706)'	183247758	C>T	108	115	'Arg194Gln[-]&Arg189Gln[-]'	No
'NOMO1(NM_014287)'	14988868	A>G	319	338	'Glu1153Gly[+]'	No
'NSUN5(NM_018044)[-]&NSUN5(NM_001168348)[-]	72722687	T>G	23	33	Not Det&Not Det&Not Det&Not Det	No
'NUMA1(NM_006185)'	71726122	T>A	83	99	'Glu809Asp[-]'	No
'OPCML(NM_001012393)&OPCML(NM_002545)'	132306610	C>T	97	107	'Ser236Asn[-]&Ser243Asn[-]'	No
'OR4B1(NM_001005470)'	48238680	G>A	129	161	'Val107Ile[+]'	No
'OR6B3(NM_173351)'	240985099	G>A	236	0	'Arg131Cys[-]'	No
'OR6Q1(NM_001005186)'	57799281	C>T	39	42	'Thr286Met[+]'	No
'OR9Q1(NM_001005212)'	57946999	T>G	138	157	'Phe28Cys[+]'	No
'ORM1(NM_000607)'	117085526	G>A	79	81	'Arg38Gln[+]'	No
'OSCP1(NM_145047)'	36898067	T>C	71	55	'Thr131Ala[-]'	No
'OXSM(NM_017897)&OXSM(NM_001145391)'	25835860	G>C	53	68	'Glu419Gln[+]&Glu336Gln[+]'	No
'PA2G4(NM_006191)'	56500381	G>A	89	96	'Arg33Gln[+]'	No
'PAM(NM_138766)&PAM(NM_138821)'	102343210	C>G	67	83	'Ser688Arg[+]&Ser581Arg[+]'	No
'PCDHA10(NM_018901)'	140237158	G>A	75	76	'Val509Met[+]'	No
'PCDHA4(NM_018907)'	140188354	C>G	94	98	'Leu528Val[+]'	No
'PCDHA4(NM_018907)'	140188709	G>T	70	86	'Arg646Leu[+]'	No
'PCDHA9(NM_031857)'	140228366	T>G	125	142	'Cys96Gly[+]'	No
'PCDHB6(NM_018939)'	140531060	G>A	148	183	'Asp408Asn[+]'	No
'PCK2(NM_004563)'	24572812	G>A	48	64	'Arg521His[+]'	No
'PDE4DIP(NM_001198834)&PDE4DIP(NM_0011988)	144879054	T>C	88	106	'Arg1466Gly[-]&Arg1422Gly[-]'	No
'PDPR(NM_017990)'	70172890	C>T	184	284	'Arg427Cys[+]'	No
'PDPR(NM_017990)'	70180088	A>T	165	303	'Tyr640Phe[+]'	No
'PDZD2(NM_178140)'	31799522	C>T	91	82	'Thr56Met[+]'	No
'PTPNM3(NM_031220)'	6441376	G>A	32	54	'Pro17Ser[-]'	No
'PIWIL2(NM_018068)'	22168668	T>A	51	48	'Met615Lys[+]'	No
'PLAC4(NM_182832)'	42551262	G>T	504	494	'His98Gln[-]'	No
'PLEKHA6(NM_014935)'	204226650	C>T	70	57	'Arg452His[-]'	No
'PLEKHG1(NM_001029884)'	151152250	A>G	43	46	'Asp668Gly[+]'	No
'PLEKHG3(NM_015549)'	65208996	C>T	14	29	'Arg865Cys[+]'	No
'PLEKHH1(NM_020715)'	68040028	G>A	82	92	'Met588Ile[+]'	No

'PM20D2(NM_001010853)'	89859108	A>G	75	82	'Tyr197Cys[+]'	No
'PMF1(NM_007221)'	156206218	C>T	36	25	'Arg170Trp[+]'	No
'POM121L12(NM_182595)'	53104052	G>A	24	20	'Val230Met[+]'	No
'POTEC(NM_001137671)'	14533105	G>C	353	282	'Ser337Cys[-]'	No
'POTED(NM_174981)'	14987871	G>T	350	367	'Asp264Tyr[+]'	No
'POTED(NM_174981)'	14987811	C>T	400	452	'His244Tyr[+]'	No
'POTED(NM_174981)'	14982886	G>A	240	441	'Gly113Ser[+]'	No
'POTEH(NM_001136213)'	16287784	C>T	294	308	'Trp34stop[-]'	No
'PPFIA4(NM_015053)[+]'	203029553	G>T	78	55	'Not Det'	No
'PPIAL4G(NM_001123068)'	143767646	G>A	150	336	'Thr68Ile[-]'	No
'PPP2R2C(NM_020416)[-]&PPP2R2C(NM_181876)[-]	6335285	C>T	80	99	'Not Det&Not Det'	No
'PRAMEF4(NM_001009611)'	12942222	C>T	28	22	'Val110Ile[-]'	No
'PRB3(NM_006249)[-]'	11421086	G>A	164	129	'Not Det'	No
'PRDX5(NM_012094)[+]&PRDX5(NM_181651)[+]&P'	64088471	C>T	79	85	'Not Det&Not Det&Not Det'	No
'PRPS1L1(NM_175886)'	18067261	G>C	266	300	'Arg49Gly[-]'	No
'PSCA(NM_005672)'	143763531	G>A	23	19	'Trp109stop[+]'	No
'PSG2(NM_031246)'	43579676	C>T	312	318	'Trp180stop[-]'	No
'PSMD13(NM_175932)'	244115	G>A	122	0	'Cys57Tyr[+]'	No
'PTPRU(NM_005704)'	29609217	G>A	72	72	'Arg633Gln[+]'	No
'PYGO1(NM_015617)'	55881002	C>T	33	42	'Gly17Ser[-]'	No
'PYHIN1(NM_198930)&PYHIN1(NM_198929)'	158911921	C>A	53	115	'Thr236Lys[+]&Thr245Lys[+]'	No
'PYROXD2(NM_032709)'	100143599	G>A	74	85	'Arg568stop[-]'	No
'RAB6C(NM_032144)'	130738163	G>A	314	340	'Ala159Thr[+]'	No
'RABEPK(NM_001174152)&RABEPK(NM_001174153)	127994947	C>T	46	42	'Ala250Val[+]&Ala199Val[+]'	No
'RALGDS(NM_001042368)[-]&RALGDS(NM_006266)'	135982143	G>A	55	71	'Not Det&Not Det'	No
'RANBP17(NM_022897)'	170692816	C>A	40	41	'His970Asn[+]'	No
'RAPSN(NM_005055)'	47463254	C>T	26	22	'Ser274Asn[-]'	No
'RASA4(NM_006989)'	102235769	T>C	15	39	'Met352Val[-]'	No
'RBM11(NM_144770)'	15593485	C>A	58	61	'Asn109Lys[+]'	No
'RBM12(NM_001198838)'	34242623	T>C	191	213	'Ile208Val[-]'	No
'REV3L(NM_002912)'	111654567	G>A	79	72	'Arg2562Cys[-]'	No
'RGPD2(NM_001078170)[+]&RGPD1(NM_00102445)'	87211874	T>C	17	27	'Not Det&Not Det'	No
'RHBDF1(NM_022450)'	108641	G>T	53	50	'Leu756Ile[-]'	No

'RICTOR(NM_152756)'	38952340	T>C	88	90	'Thr1029Ala[-]'	No
'RIN1(NM_004292)'	66103481	C>T	17	20	'Ala79Thr[-]'	No
'RNF111(NM_017610)'	59323409	A>G	151	116	'Asn130Asp[+]'	No
'RSPH10B(NM_173565)'	5983063	C>T	36	139	'Met550Ile[-]'	No
'RSPH10B(NM_173565)[-]&RSPH10B2(NM_0010996)	5998617	T>C	253	280	Not Det&Not Det'	No
'RXFP1(NM_021634)'	159567975	G>A	89	93	'Val460Met[+]'	No
'RYR3(NM_001036)'	34034616	C>T	67	62	'His2624Tyr[+]'	No
'SAC3D1(NM_013299)'	64811900	C>T	59	58	'Arg260Cys[+]'	No
'SAMD9(NM_001193307)'	92731647	G>A	35	37	'Pro1255Leu[-]'	No
'SARDH(NM_007101)'	136555623	C>T	30	25	'Gly650Arg[-]'	No
'SC4MOL(NM_006745)&SC4MOL(NM_001017369)'	166261451	G>A	136	144	'Val204Met[+]&Val73Met[+]'	No
'SCUBE2(NM_001170690)'	9088340	C>T	51	47	'Gly222Ser[-]'	No
'SERPINB3(NM_006919)'	61323259	A>T	100	90	'Trp269Arg[-]'	No
'SERPING1(NM_000062)'	57365748	C>T	9	14	'Ala2Val[+]'	No
'SHQ1(NM_018130)'	72799494	T>G	49	49	'Thr559Pro[-]'	No
'SHROOM4(NM_020717)'	50350757	T>G	39	63	'Lys1129Gln[-]'	No
'SILV(NM_006928)'	56350967	T>C	79	93	'Met374Val[-]'	No
'SIRPA(NM_001040022)'	1895951	C>T	238	0	'Leu96Phe[+]'	No
'SIRPA(NM_001040022)'	1895950	C>G	242	0	'Asp95Glu[+]'	No
'SLC14A2(NM_007163)'	43243830	G>A	52	59	'Val478Ile[+]'	No
'SLC29A4(NM_153247)'	5336713	C>T	26	14	'Arg256Cys[+]'	No
'SLC29A4(NM_153247)'	5327533	A>G	38	51	'Asp29Gly[+]'	No
'SLC29A4(NM_153247)[+]&SLC29A4(NM_00104066)	5338864	C>T	39	30	Not Det&Not Det'	No
'SLC44A2(NM_001145056)&SLC44A2(NM_020428)'	10745479	G>A	165	173	'Gly289Ser[+]&Gly291Ser[+]'	No
'SLX4(NM_032444)'	3642833	C>T	43	44	'Gly732Arg[-]'	No
'SOX7(NM_031439)'	10583616	C>T	62	69	'Gly267Ser[-]'	No
'SPATA16(NM_031955)'	172835392	A>T	225	239	'Ser44Thr[-]'	No
'SPATA3(NM_139073)'	231867427	C>T	89	113	'Arg168Cys[+]'	No
'SPDYE5(NM_001099435)'	75130916	C>A	382	520	'Ser264Tyr[+]'	No
'SPECC1L(NM_001145468)[+]&SPECC1L(NM_01533)	24698357	T>G	79	75	Not Det&Not Det'	No
'SPNS1(NM_032038)&SPNS1(NM_001142451)&SPN	28993843	C>T	98	90	'Arg378Cys[+]&Arg326Cys[+]'	No
'SPTBN5(NM_016642)'	42150888	G>A	43	39	'Thr2678Ile[-]'	No
'ST5(NM_213618)&ST5(NM_139157)'	8717982	C>T	67	61	'Arg1095Gln[-]&Arg675Gln[-]'	No

'STXBP2(NM_006949)[+]&STXBP2(NM_001127396)	7707311	C>T	78	81	Not Det&Not Det'	No
'STXBP4(NM_178509)'	53158412	G>T	59	95	'Glu453stop[+]'	No
'SVEP1(NM_153366)'	113170289	C>T	50	71	'Glu253Ilys[-]'	No
'SYCP1(NM_003176)'	115527364	C>T	52	58	'Pro860Ser[+]'	No
'SYNE1(NM_033071)&SYNE1(NM_182961)'	152665261	C>A	84	0	'Glu3989Asp[-]&Glu4060Asp[+]'	No
'SYNE1(NM_033071)&SYNE1(NM_182961)&SYNE1(	152631887	C>T	91	94	'Arg5540Gln[-]&Arg5611Gln[-]'	No
'TAF1A(NM_005681)[-]&TAF1A(NM_139352)[-]'	222734865	A>G	57	49	Not Det&Not Det'	No
'TAS2R31(NM_176885)'	11183092	C>A	170	240	'Trp281Cys[-]'	No
'TAS2R43(NM_176884)'	11244369	G>C	104	0	'Arg154Gly[-]'	No
'TAS2R43(NM_176884)'	11244230	C>A	143	14	'Cys200Phe[-]'	No
'TAS2R43(NM_176884)'	11244631	C>G	94	19	'Trp66Cys[-]'	No
'TELO2(NM_016111)'	1550409	C>T	13	17	'Pro355Leu[+]'	No
'TEP1(NM_007110)'	20863714	C>T	110	109	'Arg608Gln[-]'	No
'TFPI2(NM_006528)'	93518424	C>G	52	59	'Gly128Ala[-]'	No
'TGM3(NM_003245)'	2290333	C>A	157	0	'Thr13Lys[+]'	No
'TIMM44(NM_006351)'	8006073	C>T	70	66	'Gly19Ser[-]'	No
'TMEM132B(NM_052907)'	125900150	G>A	52	49	'Glu340Lys[+]'	No
'TMEM179B(NM_199337)'	62557511	C>T	47	48	'His218Tyr[+]'	No
'TMEM88B(NM_001146685)'	1361530	C>T	18	17	'Thr8Met[+]'	No
'TNKS1BP1(NM_033396)'	57077033	C>T	65	80	'Ser1051Asn[-]'	No
'TNXB(NM_032470)'	31977391	C>T	177	0	'Arg-170His[-]'	No
'TONSL(NM_013432)'	145662005	G>C	32	30	'Asp650Glu[-]'	No
'TPSAB1(NM_003294)'	1291597	C>G	40	1	'Asn132Lys[+]'	No
'TPSB2(NM_024164)'	1279710	G>A	17	32	'Ala-246Val[-]'	No
'TRAF3IP2(NM_147686)'	111912641	G>T	80	65	'Pro217Thr[-]'	No
'TRIM42(NM_152616)'	140397175	G>A	146	161	'Arg35Gln[+]'	No
'TRIP10(NM_004240)'	6743565	C>T	29	51	'Arg157Trp[+]'	No
'TSEN15(NM_001127394)[+]&TSEN15(NM_052965)	184021028	A>T	18	21	Not Det&Not Det'	No
'TTI1(NM_014657)'	36641471	C>T	122	116	'Glu250Lys[-]'	No
'TXNDC16(NM_001160047)'	53003450	C>T	61	65	'Ala127Thr[-]'	No
'UBE3B(NM_183415)'	109959008	G>A	65	81	'Arg711His[+]'	No
'UBR4(NM_020765)'	19479798	T>C	124	117	'Ile2277Val[-]'	No
'UGT1A7(NM_019077)'	234591148	T>C	201	223	'Tyr189His[+]'	No

'UGT2B28(NM_053039)'	70146804	G>C	151	123	'Val196Leu[+]'	No
'ULK2(NM_014683)'	19700816	G>T	46	55	'Pro568Thr[-]'	No
'UMODL1(NM_001199527)&UMODL1(NM_001199527)'	43543193	G>A	74	82	'Ser1083Asn[+]&Ser955Asn[+]'	No
'UPK1B(NM_006952)'	118906821	C>T	74	86	'Ala90Val[+]'	No
'UQCRC1(NM_003365)'	48638472	T>C	62	53	'Asn301Ser[-]'	No
'USP46(NM_001134223)[-]&USP46(NM_022832)[-]'	53476786	G>A	44	67	'Not Det&Not Det'	No
'VCX3A(NM_016379)'	6451872	C>G	104	218	'Glu159Gln[-]'	No
'VPS13D(NM_015378)'	12321134	A>G	48	57	'Thr448Ala[+]'	No
'WDFY4(NM_020945)'	50151477	G>T	68	57	'Ala2578Ser[+]'	No
'WDHD1(NM_001008396)&WDHD1(NM_007086)'	55468812	T>A	57	54	'Gln108Leu[-]&Gln231Leu[-]'	No
'WDR91(NM_014149)'	134891927	G>A	40	61	'Ala180Val[-]'	No
'WNK3(NM_001002838)[-]&WNK3(NM_020922)[-]'	54337727	G>A	108	127	'Not Det&Not Det'	No
'WWC3(NM_015691)'	10085553	C>A	9	16	'Ala485Glu[+]'	No
'XPO5(NM_020750)'	43535018	C>T	60	51	'Ser241Asn[-]'	No
'XPOT(NM_007235)'	64814251	G>A	97	90	'Glu265Lys[+]'	No
'XRCC5(NM_021141)[+]'	217005903	T>G	81	96	'Not Det'	No
'ZBBX(NM_001199202)&ZBBX(NM_001199201)'	167023573	C>T	55	68	'Ser499Asn[-]&Ser528Asn[-]'	No
'ZBED4(NM_014838)'	50277494	G>A	66	61	'Gly62Ser[+]'	No
'ZFHX4(NM_024721)'	77761269	G>C	42	31	'Ala1184Pro[+]'	No
'ZFP37(NM_003408)'	115812140	G>T	133	129	'Leu49Met[-]'	No
'ZNF235(NM_004234)'	44793164	G>C	47	41	'Gln142Glu[-]'	No
'ZNF337(NM_015655)'	25655955	C>T	129	130	'Val657Met[-]'	No
'ZNF33A(NM_006974)&ZNF33A(NM_006954)'	38345066	A>G	170	128	'Lys671Glu[+]&Lys672Glu[+]'	No
'ZNF354A(NM_005649)'	178140242	G>A	204	232	'Arg213Cys[-]'	No
'ZNF484(NM_031486)&ZNF484(NM_001007101)'	95608658	T>C	139	154	'Tyr804Cys[-]&Tyr768Cys[-]'	No
'ZNF528(NM_032423)'	52919199	G>A	84	89	'Arg365His[+]'	No
'ZNF7(NM_003416)'	146062872	C>T	84	91	'Ala76Val[+]'	No
'ZNF717(NM_001128223)'	75790513	T>C	933	0	'Tyr64Cys[-]'	No
'ZNF717(NM_001128223)'	75788010	A>C	773	0	'Val255Gly[-]'	No
'ZNF717(NM_001128223)'	75788227	A>G	502	121	'Cys183Arg[-]'	No
'ZNF717(NM_001128223)'	75788292	T>A	389	104	'Asp161Val[-]'	No
'ZNF717(NM_001128223)'	75788076	A>C	528	161	'Val233Gly[-]'	No
'ZNF717(NM_001128223)'	75787876	G>T	503	155	'Leu300Ile[-]'	No

'ZNF717(NM_001128223)'	75787869	C>T	483	159	'Cys302Tyr[-]'	No
'ZNF717(NM_001128223)'	75787870	A>G	481	159	'Cys302Arg[-]'	No
'ZNF717(NM_001128223)'	75788115	G>A	487	190	'Thr220Met[-]'	No
'ZNF717(NM_001128223)'	75788152	T>C	326	150	'Thr208Ala[-]'	No
'ZNF717(NM_001128223)'	75788226	C>A	261	123	'Cys183Phe[-]'	No
'ZNF717(NM_001128223)'	75788023	C>T	507	239	'Val251Ile[-]'	No
'ZNF717(NM_001128223)'	75786385	C>G	347	172	'Asp797His[-]'	No
'ZNF717(NM_001128223)'	75787726	G>A	500	274	'Arg350Cys[-]'	No
'ZNF717(NM_001128223)'	75787927	A>G	436	246	'Tyr283His[-]'	No
'ZNF717(NM_001128223)'	75786379	T>C	309	271	'Thr799Ala[-]'	No
'ZNF717(NM_001128223)'	75786042	G>A	483	496	'Ser911Phe[-]'	No
'ZNF717(NM_001128223)'	75786417	T>C	233	240	'Tyr786Cys[-]'	No
'ZNF717(NM_001128223)'	75786252	G>T	326	434	'Pro841His[-]'	No
'ZNF717(NM_001128223)'	75788130	C>A	273	371	'Gly215Val[-]'	No
'ZNF717(NM_001128223)'	75788434	G>T	136	192	'Gln114Lys[-]'	No
'ZNF717(NM_001128223)'	75788316	C>T	200	296	'Gly153Glu[-]'	No
'ZNF717(NM_001128223)'	75788028	G>C	269	466	'Ser249stop[-]'	No
'ZNF717(NM_001128223)'	75787519	C>A	264	487	'Gly419Trp[-]'	No
'ZNF717(NM_001128223)'	75787516	C>G	253	485	'Glu420Gln[-]'	No
'ZNF717(NM_001128223)'	75787809	T>C	260	529	'Tyr322Cys[-]'	No
'ZNF717(NM_001128223)'	75788314	T>C	155	330	'Met154Val[-]'	No
'ZNF717(NM_001128223)'	75788484	A>G	75	162	'Ile97Thr[-]'	No
'ZNF717(NM_001128223)'	75786381	T>C	182	394	'Lys798Arg[-]'	No
'ZNF717(NM_001128223)'	75787996	C>T	245	548	'Gly260Arg[-]'	No
'ZNF717(NM_001128223)'	75787962	G>C	240	537	'Thr271Ser[-]'	No
'ZNF717(NM_001128223)'	75788366	C>A	129	347	'Leu136Phe[-]'	No
'ZNF717(NM_001128223)'	75786036	A>C	200	630	'Phe913Cys[-]'	No
'ZNF717(NM_001128223)'	75787584	C>A	206	721	'Cys397Phe[-]'	No
'ZNF717(NM_001128223)'	75786073	C>G	222	778	'Glu901Gln[-]'	No
'ZNF717(NM_001128223)'	75790444	G>A	221	777	'Pro87Leu[-]'	No
'ZNF717(NM_001128223)'	75786175	C>A	181	792	'Glu867stop[-]'	No
'ZNF717(NM_001128223)'	75786202	T>C	173	762	'Ser858Gly[-]'	No
'ZNF717(NM_001128223)'	75788376	G>C	60	394	'Thr133Arg[-]'	No

'ZNF717(NM_001128223)'	75788033	A>T	97	644	'Asn247Lys[-]'	No
'ZNF717(NM_001128223)'	75788158	G>C	69	647	'Leu206Val[-]'	No
'ZNF780B(NM_001005851)'	40540724	A>C	127	105	'Val681Gly[-]'	No
'ZNF780B(NM_001005851)'	40541528	T>C	164	166	'Asp413Gly[-]'	No
'ZNF780B(NM_001005851)'	40541514	C>G	170	177	'Glu418Gln[-]'	No
'ZNF80(NM_007136)'	113955753	C>T	104	143	'Val57Met[-]'	No
'ZNF808(NM_001039886)'	53057316	C>T	146	156	'His383Tyr[+]'	No
'ZNF814(NM_001144989)'	58385748	G>A	167	385	'Ala337Val[-]'	No

**Table S12: Copy Number Alterations by patient**

Copy Number Gains in Patient 1							
Sample	Region (hg18)	Number of Exons	Reference Number of Copies	Estimated Copy Number	Copy Number Ratio	Length of Containing Segment	Informative Genes in Region
PATIENT_1	<a href="#">chrX:66681780-66860330</a>	11	1	8.5	8.5	0.18	<a href="#">AR</a>
PATIENT_1	<a href="#">chrX:67185007-67435615</a>	22	1	3.25	3.25	0.25	--
PATIENT_1	<a href="#">chrX:44705526-44944898</a>	30	1	2.33	2.33	0.24	<a href="#">KDM6A</a>
PATIENT_1	<a href="#">chrX:5837187-43626466</a>	1312	1	2.27	2.27	37.79	BMX;CASK;CDKL5;MAP3K15;PDK3; <a href="#">RPS6KA3</a>
PATIENT_1	<a href="#">chrX:49000203-52912848</a>	105	1	2.25	2.25	3.91	<a href="#">SSX2</a>
PATIENT_1	<a href="#">chrX:54796865-63407614</a>	140	1	2.23	2.23	8.61	--
PATIENT_1	<a href="#">chr10:104171786-104172645</a>	2	2	4.26	2.13	0	--
PATIENT_1	<a href="#">chr14:58827732-60021524</a>	67	2	3.96	1.98	1.19	--
PATIENT_1	<a href="#">chr13:104916660-114108638</a>	485	2	3.93	1.97	9.19	--
PATIENT_1	<a href="#">chr5:50164408-56567582</a>	296	2	3.76	1.88	6.4	IL6ST;MAP3K1
PATIENT_1	<a href="#">chr13:18646150-20649209</a>	132	2	3.7	1.85	2	<a href="#">LATS2</a>
PATIENT_1	<a href="#">chrX:53123089-54794349</a>	266	1	1.85	1.85	1.67	KDM5C;WNK3
PATIENT_1	<a href="#">chr2:174921694-174923676</a>	2	2	3.61	1.81	0	--
PATIENT_1	<a href="#">chr1:103128621-103172646</a>	13	2	3.61	1.8	0.04	--
PATIENT_1	<a href="#">chrX:2710137-5831512</a>	70	1	1.8	1.8	3.12	<a href="#">PRKX</a>
PATIENT_1	<a href="#">chr14:60259984-60512271</a>	12	2	3.52	1.76	0.25	--
PATIENT_1	<a href="#">chrX:45490583-48722620</a>	369	1	1.76	1.76	3.23	ARAF;GATA1;PIM2;SSX1;SSX4; <a href="#">WAS</a>
PATIENT_1	<a href="#">chr7:135265256-136991788</a>	40	2	3.49	1.74	1.73	--
PATIENT_1	<a href="#">chr2:133143949-134886982</a>	13	2	3.45	1.73	1.74	--
PATIENT_1	<a href="#">chr7:76092855-96648361</a>	856	2	3.36	1.68	20.56	AKAP9;CDK6;PDK4
PATIENT_1	<a href="#">chr1:16225259-16226453</a>	4	2	3.33	1.67	0	--
PATIENT_1	<a href="#">chr15:18919074-19884311</a>	16	2	3.28	1.64	0.97	--
PATIENT_1	<a href="#">chrX:48724391-48999163</a>	141	1	1.64	1.64	0.27	<a href="#">TFE3</a>
PATIENT_1	<a href="#">chr8:146248684-146250284</a>	5	2	3.21	1.6	0	--
PATIENT_1	<a href="#">chr12:104029082-104033153</a>	4	2	3.19	1.6	0	--
PATIENT_1	<a href="#">chr2:136296098-159736953</a>	448	2	3.15	1.58	23.44	ACVR1;ACVR1C;ACVR2A

PATIENT_1	<a href="#">chr2:159813198-173168872</a>	836	2	3.14	1.57	13.36	MYO3B;PDK1;STK39;TLK1
PATIENT_1	<a href="#">chr7:7240585-43646734</a>	1044	2	3.13	1.56	36.41	HNRNPA2B1;HOXA11;HOXA13;HOXA9;JAZF1; STK17A;STK31
PATIENT_1	<a href="#">chr12:10490472-10493806</a>	4	2	3.09	1.55	0	--
PATIENT_1	<a href="#">chr15:18848660-18902629</a>	3	2	3.08	1.54	0.05	--
PATIENT_1	<a href="#">chr1:150651264-151123697</a>	23	2	3	1.5	0.47	--
PATIENT_1	<a href="#">chr2:24292513-24828441</a>	46	2	2.98	1.49	0.54	<a href="#">NCOA1</a>
PATIENT_1	<a href="#">chr7:45598957-55466459</a>	232	2	2.99	1.49	9.87	<a href="#">EGFR</a>
PATIENT_1	<a href="#">chr2:75732834-85383183</a>	80	2	2.97	1.48	9.65	--
PATIENT_1	<a href="#">chr7:98999519-99344255</a>	64	2	2.92	1.46	0.34	--
PATIENT_1	<a href="#">chr7:140037055-148175264</a>	331	2	2.91	1.46	8.14	ADCK2;BRAF;EPHA1;EPHB6;EZH2; <a href="#">FLJ40852</a>
PATIENT_1	<a href="#">chr22:26525201-26580903</a>	3	2	2.91	1.46	0.06	<a href="#">MN1</a>
PATIENT_1	<a href="#">chr7:97319611-97336279</a>	11	2	2.89	1.45	0.02	--
PATIENT_1	<a href="#">chrX:43694102-44618145</a>	8	1	1.45	1.45	0.92	<a href="#">KDM6A</a>
PATIENT_1	<a href="#">chr2:31617-21119908</a>	663	2	2.88	1.44	21.09	MYCN;ROCK2;TRIB2
PATIENT_1	<a href="#">chr15:20996157-23659111</a>	122	2	2.86	1.43	2.66	--
PATIENT_1	<a href="#">chr2:174924645-242024597</a>	3834	2	2.84	1.42	67.1	ACSL3;ATIC;BMPR2;CLK1;CREB1; EPHA4;ERBB4;FEV;HOXD11;HOXD13; IDH1;NFE2L2;PASK;PAX3;PMS1; STK16;STK17B;STK36;TTN;UGT1A1
PATIENT_1	<a href="#">chr7:148551800-151577932</a>	316	2	2.84	1.42	3.03	FASTK;MLL3
PATIENT_1	<a href="#">chr7:154493912-156901426</a>	82	2	2.84	1.42	2.41	--
PATIENT_1	<a href="#">chr7:129379604-135083830</a>	348	2	2.81	1.41	5.7	--
PATIENT_1	<a href="#">chr7:157168283-158627948</a>	69	2	2.83	1.41	1.46	--
PATIENT_1	<a href="#">chr2:97121047-133142511</a>	1352	2	2.78	1.39	36.02	BUB1;ERCC3;MERTK;PAX8;TTL; <a href="#">ZAP70</a>
PATIENT_1	<a href="#">chr2:134896901-136256857</a>	102	2	2.78	1.39	1.36	<a href="#">YSK4</a>
PATIENT_1	<a href="#">chr5:43316213-50161517</a>	106	2	2.76	1.38	6.85	<a href="#">MGC42105</a>
PATIENT_1	<a href="#">chr2:85776005-96162949</a>	272	2	2.74	1.37	10.39	<a href="#">EIF2AK3</a>
PATIENT_1	<a href="#">chr6:165763793-165783779</a>	6	2	2.74	1.37	0.02	--

PATIENT_1	<a href="#">chr20:57848849-59263332</a>	70	2	2.75	1.37	1.41	--
PATIENT_1	<a href="#">chr5:126184613-129029130</a>	165	2	2.72	1.36	2.84	--
PATIENT_1	<a href="#">chr7:56137042-64975897</a>	28	2	2.7	1.35	8.84	--
PATIENT_1	<a href="#">chr7:137013890-139479866</a>	182	2	2.7	1.35	2.47	CREB3L2;TRIM24
PATIENT_1	<a href="#">chr5:158058712-159558716</a>	53	2	2.68	1.34	1.5	<a href="#">EBF1</a>
PATIENT_1	<a href="#">chr17:64375869-64822100</a>	188	2	2.67	1.34	0.45	--
PATIENT_1	<a href="#">chr11:11870142-11944009</a>	26	2	2.67	1.33	0.07	--
PATIENT_1	<a href="#">chr5:14769879-31587203</a>	99	2	2.65	1.32	16.82	--
PATIENT_1	<a href="#">chr11:55410255-55492062</a>	9	2	2.64	1.32	0.08	--
PATIENT_1	<a href="#">chr14:31101158-33470112</a>	43	2	2.64	1.32	2.37	--
PATIENT_1	<a href="#">chr3:190407972-195661897</a>	214	2	2.61	1.31	5.25	--
PATIENT_1	<a href="#">chr17:52689866-53273581</a>	15	2	2.61	1.31	0.58	<a href="#">MSI2</a>
PATIENT_1	<a href="#">chr1:94240068-103127652</a>	381	2	2.61	1.3	8.89	<a href="#">DPYD</a>
PATIENT_1	<a href="#">chr11:49124978-49178536</a>	17	2	2.61	1.3	0.05	--
PATIENT_1	<a href="#">chr11:120981102-121475718</a>	16	2	2.61	1.3	0.49	--
PATIENT_1	<a href="#">chr17:32552457-32641505</a>	21	2	2.6	1.3	0.09	--

Copy Number Losses in Patient 1							
Sample	Region (hg18)	Number of Exons	Reference Number of Copies	Estimated Copy Number	Copy Number Ratio	Length of Containing Segment	Informative Genes in Region
PATIENT_1	<a href="#">chr10:89680804-90112375</a>	10	2	0.11	0.05	0.43	<a href="#">PTEN</a>
PATIENT_1	<a href="#">chr4:185926551-185942106</a>	9	2	0.64	0.32	0.02	--
PATIENT_1	<a href="#">chr17:1498468-1533660</a>	38	2	0.81	0.4	0.04	--
PATIENT_1	<a href="#">chr18:46056031-46064365</a>	13	2	0.81	0.41	0.01	--
PATIENT_1	<a href="#">chr14:90703398-90770613</a>	12	2	0.85	0.43	0.07	--
PATIENT_1	<a href="#">chr16:79681746-79861393</a>	26	2	0.88	0.44	0.18	--
PATIENT_1	<a href="#">chr19:2024408-2061800</a>	18	2	0.87	0.44	0.04	--
PATIENT_1	<a href="#">chr9:81523581-83458739</a>	22	2	0.91	0.45	1.94	--
PATIENT_1	<a href="#">chr9:113329702-116054720</a>	259	2	0.93	0.46	2.73	--
PATIENT_1	<a href="#">chr9:116106741-117204221</a>	94	2	0.92	0.46	1.1	--
PATIENT_1	<a href="#">chr17:37212745-37283666</a>	40	2	0.93	0.46	0.07	--
PATIENT_1	<a href="#">chr18:53424913-54335256</a>	43	2	0.95	0.48	0.91	<a href="#">ALPK2</a>
PATIENT_1	<a href="#">chr19:50067097-54506208</a>	930	2	0.95	0.48	4.44	DMPK;ERCC1;ERCC2;MARK4;PRKD2
PATIENT_1	<a href="#">chr12:120563631-120683982</a>	11	2	1	0.5	0.12	--

PATIENT_1	<a href="#">chr16:67851558-69401298</a>	249	2	1	0.5	1.55	--
PATIENT_1	<a href="#">chr17:37295988-42872937</a>	969	2	1	0.5	5.58	BRCA1;ETV4;WNK4
PATIENT_1	<a href="#">chr17:63678-1497939</a>	150	2	1.02	0.51	1.43	--
PATIENT_1	<a href="#">chr1:158352281-158403758</a>	33	2	1.04	0.52	0.05	--
PATIENT_1	<a href="#">chr7:151578927-151591090</a>	4	2	1.03	0.52	0.01	<a href="#">MLL3</a>
PATIENT_1	<a href="#">chr12:56178264-56180471</a>	3	2	1.05	0.52	0	--
PATIENT_1	<a href="#">chr17:1534571-16061382</a>	2155	2	1.04	0.52	14.53	AURKB;CAMKK1;GAS7;GSG2;GUCY2D; MAP2K4;PER1;TP53;USP6
PATIENT_1	<a href="#">chr17:34116768-36926901</a>	576	2	1.06	0.53	2.81	ERBB2;LASP1;MLLT6;RARA
PATIENT_1	<a href="#">chr9:78710681-79333896</a>	81	2	1.08	0.54	0.62	--
PATIENT_1	<a href="#">chr10:67350237-89675271</a>	1162	2	1.09	0.54	22.33	BMPR1A;CAMK2G;MYST4;PRF1;PTEN
PATIENT_1	<a href="#">chr10:104223402-104225599</a>	3	2	1.08	0.54	0	--
PATIENT_1	<a href="#">chr16:71378810-79678738</a>	269	2	1.08	0.54	8.3	MAF;MLKL
PATIENT_1	<a href="#">chr22:19090611-19173384</a>	14	2	1.09	0.54	0.08	--
PATIENT_1	<a href="#">chr6:34497523-34849262</a>	25	2	1.1	0.55	0.35	--
PATIENT_1	<a href="#">chr10:377203-1411311</a>	93	2	1.09	0.55	1.03	--
PATIENT_1	<a href="#">chr15:83265263-83288849</a>	7	2	1.1	0.55	0.02	--
PATIENT_1	<a href="#">chr16:79872015-83701449</a>	233	2	1.09	0.55	3.83	--
PATIENT_1	<a href="#">chr6:43010252-43043181</a>	19	2	1.11	0.56	0.03	--
PATIENT_1	<a href="#">chr7:152128610-152182523</a>	9	2	1.12	0.56	0.05	--
PATIENT_1	<a href="#">chr13:94660991-95003118</a>	6	2	1.12	0.56	0.34	--
PATIENT_1	<a href="#">chr14:66312963-75226352</a>	750	2	1.11	0.56	8.91	GPHN;MAP3K9;NEK9;RAD51L1;RPS6KL1
PATIENT_1	<a href="#">chr14:104689064-105066361</a>	72	2	1.11	0.56	0.38	--
PATIENT_1	<a href="#">chr16:84494209-88231928</a>	258	2	1.13	0.56	3.74	<a href="#">CBFA2T3</a>
PATIENT_1	<a href="#">chr18:153440-46055496</a>	1641	2	1.13	0.56	45.9	RIOK3;ROCK1;SS18;TYMS;YES1; <a href="#">ZNF521</a>
PATIENT_1	<a href="#">chr3:125939430-126796310</a>	74	2	1.14	0.57	0.86	--
PATIENT_1	<a href="#">chr8:134323473-134325797</a>	2	2	1.15	0.57	0	--
PATIENT_1	<a href="#">chr10:93709802-94643171</a>	91	2	1.13	0.57	0.93	--
PATIENT_1	<a href="#">chr19:1439026-1997416</a>	76	2	1.14	0.57	0.56	CSNK1G2;MKNK2;TCF3
PATIENT_1	<a href="#">chr3:123604357-124649194</a>	121	2	1.17	0.58	1.04	--
PATIENT_1	<a href="#">chr21:36338025-37381499</a>	103	2	1.15	0.58	1.04	--

PATIENT_1	<a href="#">chr14:90994842-104680162</a>	1099	2	1.18	0.59	13.69	AKT1;BCL11B;CDC42BPB;DICER1;GOLGA5;  MARK3;RAGE;TCL1A;TCL6;TRIP11; <a href="#">VRK1</a>
PATIENT_1	<a href="#">chr18:46064837-53424143</a>	193	2	1.19	0.59	7.36	<a href="#">MAPK4</a>
PATIENT_1	<a href="#">chr18:54342152-76106206</a>	497	2	1.18	0.59	21.76	ALPK2;BCL2;MALT1
PATIENT_1	<a href="#">chr7:97452218-97679842</a>	18	2	1.21	0.6	0.23	<a href="#">LMTK2</a>
PATIENT_1	<a href="#">chr9:116055006-116104195</a>	26	2	1.21	0.6	0.05	--
PATIENT_1	<a href="#">chr11:3637778-3654073</a>	8	2	1.2	0.6	0.02	<a href="#">NUP98</a>
PATIENT_1	<a href="#">chr14:75319434-90696442</a>	453	2	1.2	0.6	15.38	ADCK1;RPS6KA5;TSHR
PATIENT_1	<a href="#">chr15:38494932-38653384</a>	18	2	1.21	0.6	0.16	--
PATIENT_1	<a href="#">chr9:81196266-81514395</a>	14	2	1.21	0.61	0.32	--
PATIENT_1	<a href="#">chr16:69767062-69950243</a>	6	2	1.22	0.61	0.18	--
PATIENT_1	<a href="#">chr8:106554-25821947</a>	902	2	1.23	0.62	25.72	<a href="#">BLK</a>
PATIENT_1	<a href="#">chr15:38725203-39898802</a>	242	2	1.25	0.62	1.17	LTK;TYRO3
PATIENT_1	<a href="#">chr21:38739305-46684483</a>	890	2	1.25	0.62	7.95	ERG;RIPK4;TMPRSS2
PATIENT_1	<a href="#">chr6:31214473-31226265</a>	15	2	1.26	0.63	0.01	--
PATIENT_1	<a href="#">chr6:101002795-101004241</a>	4	2	1.27	0.63	0	--
PATIENT_1	<a href="#">chr16:16015926-16077712</a>	12	2	1.27	0.63	0.06	--
PATIENT_1	<a href="#">chr16:30031880-30106242</a>	12	2	1.26	0.63	0.07	<a href="#">MAPK3</a>
PATIENT_1	<a href="#">chr9:104797491-104807842</a>	7	2	1.3	0.65	0.01	--
PATIENT_1	<a href="#">chr4:25273276-25287426</a>	12	2	1.33	0.66	0.01	--
PATIENT_1	<a href="#">chr4:187446681-191099189</a>	17	2	1.33	0.66	3.65	--
PATIENT_1	<a href="#">chr11:3789147-4001735</a>	10	2	1.32	0.66	0.21	--
PATIENT_1	<a href="#">chr11:67887884-67953681</a>	14	2	1.33	0.66	0.07	--
PATIENT_1	<a href="#">chr4:152240285-152262750</a>	9	2	1.33	0.67	0.02	--
PATIENT_1	<a href="#">chr6:89945354-89967649</a>	8	2	1.34	0.67	0.02	--
PATIENT_1	<a href="#">chr3:130457643-130467203</a>	7	2	1.37	0.68	0.01	--
PATIENT_1	<a href="#">chr6:73961376-74404899</a>	56	2	1.37	0.68	0.44	--
PATIENT_1	<a href="#">chr19:1368518-1438821</a>	34	2	1.37	0.69	0.07	--
PATIENT_1	<a href="#">chr10:94644554-94723879</a>	16	2	1.4	0.7	0.08	--
PATIENT_1	<a href="#">chr14:19911334-19911742</a>	3	2	1.4	0.7	0	--

### Copy Number Gains in Patient 2

Sample	Region (hg18)	Number of Exons	Reference Number of Copies	Estimated Copy Number	Copy Number Ratio	Length of Containing Segment	Informative Genes in Region
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PATIENT_2	<a href="#">chr15:23150629-23171853</a>	7	2	5.8	2.9	0.02	--
PATIENT_2	<a href="#">chr3:112313737-114219061</a>	162	2	5	2.5	1.91	--
PATIENT_2	<a href="#">chr3:124008440-124080857</a>	8	2	4.86	2.43	0.07	--
PATIENT_2	<a href="#">chr3:106568978-109852668</a>	145	2	4.67	2.33	3.28	<a href="#">CBLB</a>
PATIENT_2	<a href="#">chr3:114485058-115255152</a>	130	2	4.49	2.25	0.77	--
PATIENT_2	<a href="#">chr3:152500561-156691308</a>	120	2	4.47	2.23	4.19	--
PATIENT_2	<a href="#">chr3:123539134-123665528</a>	23	2	4.42	2.21	0.13	--
PATIENT_2	<a href="#">chr3:172093872-175479736</a>	116	2	4.39	2.19	3.39	--
PATIENT_2	<a href="#">chr3:121891392-122458783</a>	28	2	4.35	2.18	0.57	--
PATIENT_2	<a href="#">chr8:102281453-109070553</a>	211	2	4.36	2.18	6.79	--
PATIENT_2	<a href="#">chr7:92719962-92770752</a>	14	2	4.24	2.12	0.05	--
PATIENT_2	<a href="#">chr8:94816311-101655316</a>	394	2	4.21	2.11	6.84	<a href="#">COX6C</a>
PATIENT_2	<a href="#">chr14:23727282-23727640</a>	3	2	4	2	0	--
PATIENT_2	<a href="#">chr6:142529104-142552309</a>	4	2	3.91	1.96	0.02	--
PATIENT_2	<a href="#">chr16:13923478-14220266</a>	16	2	3.9	1.95	0.3	<a href="#">ERCC4</a>
PATIENT_2	<a href="#">chrX:83206003-83306021</a>	19	1	1.95	1.95	0.1	<a href="#">RPS6KA6</a>
PATIENT_2	<a href="#">chr3:109855764-110312302</a>	53	2	3.84	1.92	0.46	--
PATIENT_2	<a href="#">chr2:39077602-39852216</a>	69	2	3.79	1.89	0.77	CDKL4;MAP4K3
PATIENT_2	<a href="#">chr7:103588810-103628541</a>	10	2	3.77	1.89	0.04	--
PATIENT_2	<a href="#">chr8:56432891-58055228</a>	55	2	3.78	1.89	1.62	CHCHD7;LYN;MOS;PLAG1
PATIENT_2	<a href="#">chr16:7508270-7661580</a>	8	2	3.77	1.88	0.15	--
PATIENT_2	<a href="#">chr2:11241015-11345272</a>	32	2	3.73	1.86	0.1	<a href="#">ROCK2</a>
PATIENT_2	<a href="#">chr20:57844982-57929831</a>	46	2	3.72	1.86	0.08	--
PATIENT_2	<a href="#">chr1:161562526-163028553</a>	16	2	3.66	1.83	1.47	<a href="#">PBX1</a>
PATIENT_2	<a href="#">chr1:205999649-206030246</a>	10	2	3.62	1.81	0.03	--
PATIENT_2	<a href="#">chr5:38988896-39351760</a>	33	2	3.61	1.81	0.36	--
PATIENT_2	<a href="#">chr6:119611170-121662320</a>	28	2	3.62	1.81	2.05	--
PATIENT_2	<a href="#">chr3:73129958-89611289</a>	120	2	3.6	1.8	16.48	<a href="#">EPHA3</a>
PATIENT_2	<a href="#">chr5:127499344-127548413</a>	20	2	3.6	1.8	0.05	--
PATIENT_2	<a href="#">chr9:104797491-105941328</a>	31	2	3.6	1.8	1.14	--
PATIENT_2	<a href="#">chr12:37382966-39047773</a>	132	2	3.6	1.8	1.66	<a href="#">LRRK2</a>
PATIENT_2	<a href="#">chr3:122869646-123189924</a>	60	2	3.56	1.78	0.32	--

PATIENT_2	<a href="#">chr10:32791626-33183378</a>	31	2	3.56	1.78	0.39	--
PATIENT_2	<a href="#">chr1:165225643-165252113</a>	8	2	3.54	1.77	0.03	--
PATIENT_2	<a href="#">chr2:20750239-21106333</a>	25	2	3.53	1.77	0.36	--
PATIENT_2	<a href="#">chr3:123257033-123526862</a>	14	2	3.54	1.77	0.27	--
PATIENT_2	<a href="#">chr18:28926797-29231140</a>	17	2	3.53	1.77	0.3	--
PATIENT_2	<a href="#">chr3:175481375-184495870</a>	232	2	3.52	1.76	9.01	PIK3CA;SOX2
PATIENT_2	<a href="#">chr2:24323217-24806030</a>	39	2	3.5	1.75	0.48	<a href="#">NCOA1</a>
PATIENT_2	<a href="#">chr5:74905384-74929556</a>	11	2	3.48	1.74	0.02	--
PATIENT_2	<a href="#">chr10:14921949-14936207</a>	8	2	3.47	1.74	0.01	--
PATIENT_2	<a href="#">chr3:45843903-45854484</a>	8	2	3.45	1.73	0.01	--
PATIENT_2	<a href="#">chr16:1824312-1929129</a>	6	2	3.47	1.73	0.1	--
PATIENT_2	<a href="#">chr9:79017734-79189306</a>	61	2	3.44	1.72	0.17	--
PATIENT_2	<a href="#">chr10:22211295-22658022</a>	22	2	3.44	1.72	0.45	--
PATIENT_2	<a href="#">chr3:39082344-39110464</a>	16	2	3.42	1.71	0.03	--
PATIENT_2	<a href="#">chr7:104509425-104534876</a>	9	2	3.43	1.71	0.03	--
PATIENT_2	<a href="#">chr10:37465572-37560398</a>	24	2	3.43	1.71	0.09	--
PATIENT_2	<a href="#">chr2:11825387-20701784</a>	238	2	3.39	1.7	8.88	MYCN;TRIB2
PATIENT_2	<a href="#">chr3:33828594-35733823</a>	29	2	3.4	1.7	1.91	--
PATIENT_2	<a href="#">chr6:97687296-97835896</a>	25	2	3.4	1.7	0.15	--
PATIENT_2	<a href="#">chr12:21907204-21916878</a>	3	2	3.4	1.7	0.01	--
PATIENT_2	<a href="#">chr12:10351946-10762977</a>	59	2	3.38	1.69	0.41	<a href="#">STYK1</a>
PATIENT_2	<a href="#">chr13:35646932-35665973</a>	5	2	3.38	1.69	0.02	--
PATIENT_2	<a href="#">chr2:31617-662834</a>	18	2	3.36	1.68	0.63	--
PATIENT_2	<a href="#">chr3:122460642-122746344</a>	40	2	3.35	1.68	0.29	--
PATIENT_2	<a href="#">chr10:82085906-82172198</a>	11	2	3.36	1.68	0.09	--
PATIENT_2	<a href="#">chr12:1733855-1977381</a>	18	2	3.36	1.68	0.24	--
PATIENT_2	<a href="#">chr15:18848660-23136396</a>	181	2	3.36	1.68	4.29	--
PATIENT_2	<a href="#">chr11:49124978-49184247</a>	18	2	3.33	1.67	0.06	--
PATIENT_2	<a href="#">chr15:23201701-23659111</a>	22	2	3.33	1.67	0.46	--
PATIENT_2	<a href="#">chr16:2078529-2084032</a>	9	2	3.33	1.67	0.01	<a href="#">TSC2</a>
PATIENT_2	<a href="#">chr16:21876098-21907518</a>	15	2	3.35	1.67	0.03	--
PATIENT_2	<a href="#">chrX:149578840-149650674</a>	11	1	1.67	1.67	0.07	--
PATIENT_2	<a href="#">chr3:8898091-9007359</a>	15	2	3.3	1.65	0.11	<a href="#">SRGAP3</a>
PATIENT_2	<a href="#">chr3:14670988-14687555</a>	10	2	3.3	1.65	0.02	--

PATIENT_2	<a href="#">chr3:130470114-134430865</a>	327	2	3.3	1.65	3.96	NEK11;PIK3R4
PATIENT_2	<a href="#">chr3:156693273-171727267</a>	459	2	3.29	1.65	15.03	MLF1;PRKCI
PATIENT_2	<a href="#">chr11:20367906-20472332</a>	13	2	3.29	1.65	0.1	--
PATIENT_2	<a href="#">chr1:84185484-84442756</a>	14	2	3.28	1.64	0.26	<a href="#">PRKACB</a>
PATIENT_2	<a href="#">chr16:65394467-65416273</a>	17	2	3.29	1.64	0.02	--
PATIENT_2	<a href="#">chr1:225270462-225909405</a>	35	2	3.26	1.63	0.64	<a href="#">CDC42BPA</a>
PATIENT_2	<a href="#">chr6:91283030-97107990</a>	57	2	3.27	1.63	5.82	EPHA7;MAP3K7
PATIENT_2	<a href="#">chr12:23648662-29411111</a>	266	2	3.26	1.63	5.76	KRAS;STK38L
PATIENT_2	<a href="#">chrX:137649083-138736588</a>	61	1	1.63	1.63	1.09	--
PATIENT_2	<a href="#">chr3:130322920-130456238</a>	21	2	3.24	1.62	0.13	--
PATIENT_2	<a href="#">chr16:24103972-24735707</a>	48	2	3.23	1.62	0.63	--
PATIENT_2	<a href="#">chr2:26271534-26507200</a>	35	2	3.23	1.61	0.24	--
PATIENT_2	<a href="#">chr3:124111758-130086244</a>	466	2	3.22	1.61	5.97	GATA2;KALRN;MYLK;RPN1
PATIENT_2	<a href="#">chr8:38984610-40508906</a>	63	2	3.23	1.61	1.52	--
PATIENT_2	<a href="#">chr2:43725437-43905596</a>	49	2	3.21	1.6	0.18	--
PATIENT_2	<a href="#">chr2:55053816-64064569</a>	455	2	3.19	1.6	9.01	BCL11A;REL;VRK2
PATIENT_2	<a href="#">chr16:21234762-21598019</a>	16	2	3.2	1.6	0.36	--
PATIENT_2	<a href="#">chr1:203954130-203965347</a>	6	2	3.18	1.59	0.01	--
PATIENT_2	<a href="#">chr2:42326239-42433921</a>	24	2	3.18	1.59	0.11	<a href="#">EML4</a>
PATIENT_2	<a href="#">chr3:114451387-114482628</a>	13	2	3.18	1.59	0.03	--
PATIENT_2	<a href="#">chr3:115257958-121883640</a>	193	2	3.18	1.59	6.63	<a href="#">GSK3B</a>
PATIENT_2	<a href="#">chr3:123668912-123996980</a>	34	2	3.18	1.59	0.33	--
PATIENT_2	<a href="#">chr2:43969270-45686044</a>	101	2	3.16	1.58	1.72	--
PATIENT_2	<a href="#">chr1:182209439-199093657</a>	643	2	3.13	1.57	16.88	NEK7;PTGS2;TPR
PATIENT_2	<a href="#">chr2:46695693-46704837</a>	5	2	3.14	1.57	0.01	--
PATIENT_2	<a href="#">chr6:38420792-39088296</a>	96	2	3.14	1.57	0.67	--
PATIENT_2	<a href="#">chr17:30279214-30310750</a>	13	2	3.14	1.57	0.03	--
PATIENT_2	<a href="#">chr1:233946655-234060244</a>	39	2	3.11	1.56	0.11	--
PATIENT_2	<a href="#">chr9:125454167-125594708</a>	7	2	3.11	1.56	0.14	--
PATIENT_2	<a href="#">chr11:73727236-73763192</a>	12	2	3.11	1.56	0.04	--
PATIENT_2	<a href="#">chr12:4469982-4535854</a>	20	2	3.12	1.56	0.07	--
PATIENT_2	<a href="#">chrX:18949189-19277380</a>	12	1	1.56	1.56	0.33	--
PATIENT_2	<a href="#">chr3:9721290-9721626</a>	3	2	3.1	1.55	0	--

PATIENT_2	<a href="#">chr1:166155896-166321525</a>	24	2	3.08	1.54	0.17	--
PATIENT_2	<a href="#">chr3:5187227-5223897</a>	12	2	3.09	1.54	0.04	--
PATIENT_2	<a href="#">chr8:42321660-42334030</a>	7	2	3.07	1.54	0.01	<a href="#">POLB</a>
PATIENT_2	<a href="#">chr11:124995895-125030377</a>	13	2	3.08	1.54	0.03	<a href="#">CHEK1</a>
PATIENT_2	<a href="#">chr11:133569806-133595752</a>	13	2	3.08	1.54	0.03	--
PATIENT_2	<a href="#">chr14:59973416-60021524</a>	17	2	3.07	1.54	0.05	--
PATIENT_2	<a href="#">chr6:169846066-169917328</a>	27	2	3.07	1.53	0.07	--
PATIENT_2	<a href="#">chr8:30689133-32726632</a>	56	2	3.07	1.53	2.04	<a href="#">WRN</a>
PATIENT_2	<a href="#">chr2:11401642-11514782</a>	7	2	3.03	1.52	0.11	<a href="#">ROCK2</a>
PATIENT_2	<a href="#">chr2:67479868-68126990</a>	8	2	3.03	1.52	0.65	--
PATIENT_2	<a href="#">chr3:336504-3191899</a>	98	2	3.05	1.52	2.86	--
PATIENT_2	<a href="#">chr3:15101326-15267698</a>	25	2	3.04	1.52	0.17	--
PATIENT_2	<a href="#">chr10:76642027-76982269</a>	14	2	3.03	1.52	0.34	--
PATIENT_2	<a href="#">chr14:24513847-30241292</a>	55	2	3.04	1.52	5.73	<a href="#">PRKD1</a>
PATIENT_2	<a href="#">chr18:74971417-75138112</a>	11	2	3.04	1.52	0.17	--
PATIENT_2	<a href="#">chr20:60318946-60320926</a>	5	2	3.04	1.52	0	--
PATIENT_2	<a href="#">chr21:13909675-26175902</a>	154	2	3.03	1.52	12.27	--
PATIENT_2	<a href="#">chr2:40196104-40510080</a>	10	2	3.01	1.51	0.31	--
PATIENT_2	<a href="#">chr7:76634999-92707148</a>	616	2	3.01	1.51	16.07	AKAP9;CDK6
PATIENT_2	<a href="#">chr17:4985480-4991157</a>	7	2	3.01	1.51	0.01	<a href="#">USP6</a>
PATIENT_2	<a href="#">chr20:55338395-55497232</a>	26	2	3.02	1.51	0.16	--
PATIENT_2	<a href="#">chr2:31423175-39075899</a>	387	2	2.99	1.5	7.65	EIF2AK2;PRKD3
PATIENT_2	<a href="#">chr2:71450581-71509236</a>	18	2	3	1.5	0.06	--
PATIENT_2	<a href="#">chr6:74489708-89928623</a>	564	2	3	1.5	15.44	<a href="#">TTK</a>
PATIENT_2	<a href="#">chr11:75240634-75529753</a>	13	2	3.01	1.5	0.29	--
PATIENT_2	<a href="#">chrX:153936102-154428040</a>	25	1	1.5	1.5	0.49	<a href="#">MTCP1</a>
PATIENT_2	<a href="#">chr2:65320544-65341957</a>	6	2	2.98	1.49	0.02	--
PATIENT_2	<a href="#">chr3:45719982-45775548</a>	20	2	2.98	1.49	0.06	--
PATIENT_2	<a href="#">chr3:139677807-152495167</a>	543	2	2.99	1.49	12.82	ATR;FOXL2;GRK7
PATIENT_2	<a href="#">chr6:52649894-73959071</a>	435	2	2.97	1.49	21.31	<a href="#">ICK</a>
PATIENT_2	<a href="#">chr7:92773163-97331625</a>	233	2	2.99	1.49	4.56	<a href="#">PDK4</a>
PATIENT_2	<a href="#">chr9:97282591-97768743</a>	19	2	2.98	1.49	0.49	--
PATIENT_2	<a href="#">chrX:146811168-147852051</a>	33	1	1.49	1.49	1.04	--
PATIENT_2	<a href="#">chr12:3791707-3809379</a>	7	2	2.97	1.48	0.02	--

PATIENT_2	<a href="#">chr13:32120963-32214796</a>	22	2	2.97	1.48	0.09	--
PATIENT_2	<a href="#">chr18:37821816-40703219</a>	32	2	2.96	1.48	2.88	--
PATIENT_2	<a href="#">chr21:29170630-29363654</a>	71	2	2.96	1.48	0.19	--
PATIENT_2	<a href="#">chr21:32933197-33058608</a>	47	2	2.97	1.48	0.13	--
PATIENT_2	<a href="#">chr1:166427271-166472602</a>	9	2	2.94	1.47	0.05	--
PATIENT_2	<a href="#">chr3:16277307-31652519</a>	290	2	2.93	1.47	15.38	NEK10;TGFBR2
PATIENT_2	<a href="#">chr3:32500524-32749979</a>	25	2	2.93	1.47	0.25	--
PATIENT_2	<a href="#">chr3:38199553-38266486</a>	14	2	2.93	1.47	0.07	<a href="#">OXSR1</a>
PATIENT_2	<a href="#">chr7:38433094-38904234</a>	42	2	2.95	1.47	0.47	--
PATIENT_2	<a href="#">chr6:39421498-39796510</a>	19	2	2.92	1.46	0.38	--
PATIENT_2	<a href="#">chr12:8216494-8221153</a>	5	2	2.93	1.46	0	--
PATIENT_2	<a href="#">chr1:234413764-234833947</a>	77	2	2.89	1.45	0.42	--
PATIENT_2	<a href="#">chr3:196481395-196725005</a>	23	2	2.91	1.45	0.24	--
PATIENT_2	<a href="#">chr5:153170877-153394601</a>	14	2	2.89	1.45	0.22	--
PATIENT_2	<a href="#">chr7:105520724-126813397</a>	669	2	2.9	1.45	21.29	<a href="#">MET</a>
PATIENT_2	<a href="#">chr10:95431285-95449814</a>	10	2	2.9	1.45	0.02	--
PATIENT_2	<a href="#">chr11:22181948-34102473</a>	366	2	2.89	1.45	11.92	FANCF;HIPK3;LMO2;WT1
PATIENT_2	<a href="#">chr11:77867148-93180390</a>	328	2	2.89	1.45	15.31	<a href="#">PICALM</a>
PATIENT_2	<a href="#">chr11:113777710-114585623</a>	24	2	2.9	1.45	0.81	--
PATIENT_2	<a href="#">chr1:64443950-64479963</a>	7	2	2.87	1.44	0.04	--
PATIENT_2	<a href="#">chr1:232586139-233565237</a>	75	2	2.88	1.44	0.98	--
PATIENT_2	<a href="#">chr2:27655920-31022196</a>	223	2	2.89	1.44	3.37	<a href="#">ALK</a>
PATIENT_2	<a href="#">chr3:9141504-9400957</a>	10	2	2.88	1.44	0.26	<a href="#">SRGAP3</a>
PATIENT_2	<a href="#">chr6:90099583-90416550</a>	21	2	2.89	1.44	0.32	--
PATIENT_2	<a href="#">chr16:8895952-11852817</a>	149	2	2.87	1.44	2.96	C16orf75;CIITA;SOCS1
PATIENT_2	<a href="#">chr20:48985127-49005179</a>	8	2	2.87	1.44	0.02	--
PATIENT_2	<a href="#">chr3:198255943-198507679</a>	25	2	2.86	1.43	0.25	--
PATIENT_2	<a href="#">chr6:44444153-52121738</a>	327	2	2.87	1.43	7.68	--
PATIENT_2	<a href="#">chr6:109895574-119567684</a>	486	2	2.87	1.43	9.67	FRK;FYN;GOPC;ROS1
PATIENT_2	<a href="#">chr9:99427941-99800719</a>	42	2	2.87	1.43	0.37	<a href="#">XPA</a>
PATIENT_2	<a href="#">chr1:150750634-151066800</a>	23	2	2.84	1.42	0.32	--
PATIENT_2	<a href="#">chr2:47210603-54385385</a>	206	2	2.84	1.42	7.17	MSH2;MSH6
PATIENT_2	<a href="#">chr2:75727492-85214681</a>	79	2	2.85	1.42	9.49	--

PATIENT_2	<a href="#">chr3:7315441-8553998</a>	12	2	2.83	1.42	1.24	--
PATIENT_2	<a href="#">chr5:79414054-112376998</a>	805	2	2.83	1.42	32.96	APC;CAMK4;FER;RIOK2
PATIENT_2	<a href="#">chr1:115201397-115339094</a>	25	2	2.82	1.41	0.14	--
PATIENT_2	<a href="#">chr2:208887304-215711141</a>	266	2	2.82	1.41	6.82	<a href="#">ERBB4</a>
PATIENT_2	<a href="#">chr5:112878912-122977961</a>	274	2	2.82	1.41	10.1	<a href="#">CSNK1G3</a>
PATIENT_2	<a href="#">chr17:3290286-3363998</a>	15	2	2.82	1.41	0.07	--
PATIENT_2	<a href="#">chr1:148933846-148986927</a>	16	2	2.81	1.4	0.05	--
PATIENT_2	<a href="#">chr2:222007180-224350740</a>	66	2	2.8	1.4	2.34	ACSL3;EPHA4;PAX3
PATIENT_2	<a href="#">chr2:230749654-231446445</a>	80	2	2.79	1.4	0.7	--
PATIENT_2	<a href="#">chr3:189606698-195662762</a>	224	2	2.81	1.4	6.06	<a href="#">LPP</a>
PATIENT_2	<a href="#">chr5:14654153-14743270</a>	12	2	2.8	1.4	0.09	--
PATIENT_2	<a href="#">chr6:121666533-142510173</a>	755	2	2.8	1.4	20.84	MAP3K5;MYB;TNFAIP3
PATIENT_2	<a href="#">chr17:28063230-28129657</a>	14	2	2.79	1.4	0.07	--
PATIENT_2	<a href="#">chr21:31960667-32234375</a>	25	2	2.8	1.4	0.27	<a href="#">HUNK</a>
PATIENT_2	<a href="#">chr3:37767010-37992296</a>	13	2	2.78	1.39	0.23	--
PATIENT_2	<a href="#">chr5:39367603-71778912</a>	979	2	2.78	1.39	32.41	CDK7;IL6ST;MAP3K1;MGC42105;PIK3R1;  PLK2;PRKAA1
PATIENT_2	<a href="#">chr9:36042287-36098066</a>	13	2	2.77	1.39	0.06	--
PATIENT_2	<a href="#">chr11:93792966-113307744</a>	727	2	2.78	1.39	19.51	ATM;BIRC3;DDX10;PGR;POU2AF1;  <a href="#">SDHD</a>
PATIENT_2	<a href="#">chr18:54967779-55254236</a>	27	2	2.79	1.39	0.29	--
PATIENT_2	<a href="#">chr20:5486670-10569826</a>	208	2	2.77	1.39	5.08	<a href="#">PAK7</a>
PATIENT_2	<a href="#">chrX:10397808-15186948</a>	161	1	1.39	1.39	4.79	--
PATIENT_2	<a href="#">chr2:224490937-230452990</a>	248	2	2.76	1.38	5.96	--
PATIENT_2	<a href="#">chr3:122747332-122869079</a>	23	2	2.77	1.38	0.12	--
PATIENT_2	<a href="#">chr8:49125028-56178160</a>	120	2	2.76	1.38	7.05	--
PATIENT_2	<a href="#">chr9:130493298-130496752</a>	6	2	2.76	1.38	0	<a href="#">SET</a>
PATIENT_2	<a href="#">chr11:59377054-60232764</a>	80	2	2.76	1.38	0.86	--
PATIENT_2	<a href="#">chr12:66835484-87463716</a>	601	2	2.75	1.38	20.63	<a href="#">MDM2</a>
PATIENT_2	<a href="#">chr18:58029412-69976642</a>	261	2	2.77	1.38	11.95	<a href="#">BCL2</a>
PATIENT_2	<a href="#">chr1:90236278-90265854</a>	12	2	2.74	1.37	0.03	--
PATIENT_2	<a href="#">chr6:97836992-109869042</a>	361	2	2.74	1.37	12.03	<a href="#">PRDM1</a>

PATIENT_2	<a href="#">chr6:167716319-168091914</a>	29	2	2.74	1.37	0.38	<a href="#">MLLT4</a>
PATIENT_2	<a href="#">chr9:19280827-19369550</a>	32	2	2.74	1.37	0.09	--
PATIENT_2	<a href="#">chr10:75428055-76418829</a>	52	2	2.74	1.37	0.99	<a href="#">MYST4</a>
PATIENT_2	<a href="#">chr11:19034028-19862449</a>	26	2	2.75	1.37	0.83	--
PATIENT_2	<a href="#">chr20:36555087-36636927</a>	28	2	2.74	1.37	0.08	--
PATIENT_2	<a href="#">chr1:86145491-86625241</a>	44	2	2.72	1.36	0.48	--
PATIENT_2	<a href="#">chr1:210685882-224037658</a>	618	2	2.73	1.36	13.35	MARK1;RPS6KC1
PATIENT_2	<a href="#">chr3:110315947-110539027</a>	15	2	2.72	1.36	0.22	--
PATIENT_2	<a href="#">chr5:160685998-162877201</a>	70	2	2.72	1.36	2.19	--
PATIENT_2	<a href="#">chr6:6167333-6599817</a>	12	2	2.72	1.36	0.43	--
PATIENT_2	<a href="#">chr9:100857229-103539732</a>	146	2	2.72	1.36	2.68	NR4A3;TGFBR1
PATIENT_2	<a href="#">chr1:235040464-245389674</a>	332	2	2.69	1.35	10.35	AKT3;FH
PATIENT_2	<a href="#">chr2:86162287-86925573</a>	93	2	2.71	1.35	0.76	--
PATIENT_2	<a href="#">chr4:186576621-186620823</a>	8	2	2.69	1.35	0.04	--
PATIENT_2	<a href="#">chr6:32368754-32447454</a>	23	2	2.7	1.35	0.08	--
PATIENT_2	<a href="#">chr6:166834383-167625010</a>	30	2	2.69	1.35	0.79	FGFR1OP;RPS6KA2
PATIENT_2	<a href="#">chr9:19540200-33024270</a>	262	2	2.7	1.35	13.48	CDKN2A;MLLT3;TAF1L;TEK
PATIENT_2	<a href="#">chr11:58052165-58735838</a>	43	2	2.7	1.35	0.68	--
PATIENT_2	<a href="#">chr12:31326992-37373816</a>	95	2	2.69	1.35	6.05	--
PATIENT_2	<a href="#">chrX:118856437-128703801</a>	269	1	1.35	1.35	9.85	--
PATIENT_2	<a href="#">chr2:665569-11235359</a>	290	2	2.69	1.34	10.57	--
PATIENT_2	<a href="#">chr5:14769879-38988169</a>	613	2	2.69	1.34	24.22	<a href="#">LIFR</a>
PATIENT_2	<a href="#">chr5:126812751-127497810</a>	19	2	2.68	1.34	0.69	--
PATIENT_2	<a href="#">chr8:106554-655933</a>	21	2	2.68	1.34	0.55	--
PATIENT_2	<a href="#">chr10:71575826-71660131</a>	18	2	2.67	1.34	0.08	--
PATIENT_2	<a href="#">chr14:91220006-91406401</a>	22	2	2.68	1.34	0.19	--
PATIENT_2	<a href="#">chr20:47108449-47144791</a>	23	2	2.68	1.34	0.04	--
PATIENT_2	<a href="#">chr2:231451012-231829559</a>	37	2	2.66	1.33	0.38	--
PATIENT_2	<a href="#">chr3:35738215-37451554</a>	93	2	2.65	1.33	1.71	<a href="#">MLH1</a>
PATIENT_2	<a href="#">chr3:184497553-188930017</a>	548	2	2.66	1.33	4.43	BCL6;EIF4A2;EPHB3;ETV5;MAP3K13
PATIENT_2	<a href="#">chr4:107353398-107468113</a>	19	2	2.66	1.33	0.11	--
PATIENT_2	<a href="#">chr5:159709059-159788226</a>	29	2	2.66	1.33	0.08	--
PATIENT_2	<a href="#">chr5:179597973-179628950</a>	10	2	2.66	1.33	0.03	<a href="#">MAPK9</a>

PATIENT_2	<a href="#">chr8:113310204-114518170</a>	71	2	2.66	1.33	1.21	--
PATIENT_2	<a href="#">chr9:3916017-79015381</a>	398	2	2.67	1.33	39.85	PRKACG;TRPM6
PATIENT_2	<a href="#">chr10:94643171-94723879</a>	17	2	2.65	1.33	0.08	--
PATIENT_2	<a href="#">chr11:226184-234447</a>	6	2	2.66	1.33	0.01	--
PATIENT_2	<a href="#">chr16:14235572-21197010</a>	616	2	2.66	1.33	6.96	<a href="#">MYH11</a>
PATIENT_2	<a href="#">chr20:32460188-32559210</a>	23	2	2.66	1.33	0.1	--
PATIENT_2	<a href="#">chr3:47059124-47138147</a>	15	2	2.65	1.32	0.08	<a href="#">SETD2</a>
PATIENT_2	<a href="#">chr5:137241158-137381995</a>	40	2	2.63	1.32	0.14	--
PATIENT_2	<a href="#">chr6:249612-601525</a>	42	2	2.63	1.32	0.35	<a href="#">IRF4</a>
PATIENT_2	<a href="#">chr7:129826041-130822966</a>	50	2	2.64	1.32	1	--
PATIENT_2	<a href="#">chr8:41911402-42139024</a>	19	2	2.63	1.32	0.23	--
PATIENT_2	<a href="#">chr8:109163995-110645903</a>	48	2	2.64	1.32	1.48	--
PATIENT_2	<a href="#">chr9:107459-19086719</a>	585	2	2.64	1.32	18.98	CD274;JAK2;NFIB
PATIENT_2	<a href="#">chr10:15599205-22134974</a>	301	2	2.63	1.32	6.54	<a href="#">MLLT10</a>
PATIENT_2	<a href="#">chr10:22658312-32785226</a>	488	2	2.63	1.32	10.13	MAP3K8;MASTL;MYO3A
PATIENT_2	<a href="#">chr17:29607412-29712972</a>	16	2	2.64	1.32	0.11	--
PATIENT_2	<a href="#">chr20:51621744-54396639</a>	51	2	2.64	1.32	2.77	<a href="#">AURKA</a>
PATIENT_2	<a href="#">chrX:15242470-18556519</a>	213	1	1.32	1.32	3.31	BMX;CDKL5
PATIENT_2	<a href="#">chr1:205294727-205997558</a>	62	2	2.61	1.31	0.7	--
PATIENT_2	<a href="#">chr2:182469026-19644209</a>	608	2	2.62	1.31	14.38	PMS1;STK17B
PATIENT_2	<a href="#">chr2:219032814-219165319</a>	25	2	2.62	1.31	0.13	--
PATIENT_2	<a href="#">chr4:191101290-191121259</a>	9	2	2.62	1.31	0.02	--
PATIENT_2	<a href="#">chr5:74016990-74900996</a>	92	2	2.61	1.31	0.88	--
PATIENT_2	<a href="#">chr5:76362535-79371757</a>	156	2	2.61	1.31	3.01	--
PATIENT_2	<a href="#">chr6:3976818-4949173</a>	50	2	2.61	1.31	0.97	<a href="#">PRPF4B</a>
PATIENT_2	<a href="#">chr7:102282501-103564519</a>	155	2	2.63	1.31	1.28	--
PATIENT_2	<a href="#">chr8:42880515-48483025</a>	49	2	2.61	1.31	5.6	<a href="#">HOOK3</a>
PATIENT_2	<a href="#">chr11:34417169-43870210</a>	178	2	2.62	1.31	9.45	--
PATIENT_2	<a href="#">chr11:75740520-76408992</a>	37	2	2.62	1.31	0.67	--
PATIENT_2	<a href="#">chr12:119705898-119901117</a>	5	2	2.62	1.31	0.2	--
PATIENT_2	<a href="#">chrX:19674418-46194846</a>	715	1	1.31	1.31	26.52	CASK;KDM6A;PDK3;RPS6KA3
PATIENT_2	<a href="#">chrX:134821590-137620737</a>	130	1	1.31	1.31	2.8	--
PATIENT_2	<a href="#">chr1:167347295-181187150</a>	800	2	2.6	1.3	13.84	ABL2;RNASEL;SCYL3
PATIENT_2	<a href="#">chr7:57192144-64858014</a>	23	2	2.61	1.3	7.67	--

PATIENT_2	<a href="#">chr8:121477534-121604737</a>	29	2	2.6	1.3	0.13	--
PATIENT_2	<a href="#">chr10:51135207-70637628</a>	556	2	2.61	1.3	19.5	NCOA4;PRKG1
PATIENT_2	<a href="#">chr13:20046566-20163253</a>	25	2	2.6	1.3	0.12	--
PATIENT_2	<a href="#">chrX:129166789-134543172</a>	213	1	1.3	1.3	5.38	<a href="#">GPC3</a>

Copy Number Losses in Patient 2							
Sample	Region (hg18)	Number of Exons	Reference Number of Copies	Estimated Copy Number	Copy Number Ratio	Length of Containing Segment	Informative Genes in Region
PATIENT_2	<a href="#">chr10:89504483-89715116</a>	18	2	0.18	0.09	0.21	<a href="#">PTEN</a>
PATIENT_2	<a href="#">chr2:96061564-96061802</a>	2	2	0.37	0.19	0	--
PATIENT_2	<a href="#">chr17:7571249-7614885</a>	24	2	0.45	0.22	0.04	--
PATIENT_2	<a href="#">chr17:7615441-8006351</a>	246	2	0.56	0.28	0.39	GUCY2D;PER1
PATIENT_2	<a href="#">chr17:10387798-11813455</a>	124	2	0.56	0.28	1.43	--
PATIENT_2	<a href="#">chr22:34991583-35020186</a>	15	2	0.6	0.3	0.03	<a href="#">MYH9</a>
PATIENT_2	<a href="#">chr17:7533688-7567701</a>	15	2	0.66	0.33	0.03	--
PATIENT_2	<a href="#">chr17:11822392-14624061</a>	69	2	0.7	0.35	2.8	<a href="#">MAP2K4</a>
PATIENT_2	<a href="#">chr10:90024733-90112375</a>	4	2	0.78	0.39	0.09	--
PATIENT_2	<a href="#">chr16:57258840-57308142</a>	14	2	0.79	0.4	0.05	--
PATIENT_2	<a href="#">chr15:38830987-38953202</a>	43	2	0.86	0.43	0.12	--
PATIENT_2	<a href="#">chr11:826346-828162</a>	6	2	0.88	0.44	0	--
PATIENT_2	<a href="#">chr12:51801402-51840270</a>	8	2	0.87	0.44	0.04	--
PATIENT_2	<a href="#">chr19:43913588-44580057</a>	175	2	0.87	0.44	0.67	<a href="#">PAK4</a>
PATIENT_2	<a href="#">chr17:24098383-24818324</a>	68	2	0.92	0.46	0.72	<a href="#">TAOK1</a>
PATIENT_2	<a href="#">chr19:7026100-11413113</a>	937	2	0.94	0.47	4.39	DNMT1;INSR;MAP2K7;SMARCA4;TYK2
PATIENT_2	<a href="#">chr1:25574466-25607853</a>	7	2	0.96	0.48	0.03	--
PATIENT_2	<a href="#">chr3:53132837-53251239</a>	32	2	0.96	0.48	0.12	<a href="#">PRKCD</a>
PATIENT_2	<a href="#">chr15:87822140-87840687</a>	6	2	0.96	0.48	0.02	--
PATIENT_2	<a href="#">chr16:67701117-69248444</a>	242	2	0.97	0.48	1.55	--
PATIENT_2	<a href="#">chr17:2791139-7533315</a>	113	2	0.96	0.48	0.24	<a href="#">TP53</a>
PATIENT_2	<a href="#">chr17:24842964-24999387</a>	61	2	0.99	0.49	0.16	<a href="#">TAOK1</a>
PATIENT_2	<a href="#">chr2:96153526-98175861</a>	185	2	1	0.5	2.02	TMEM127;ZAP70
PATIENT_2	<a href="#">chr3:48601260-52538297</a>	937	2	1	0.5	3.94	BAP1;CAMKV;MAPKAPK3;MST1R
PATIENT_2	<a href="#">chr4:71773356-71807250</a>	4	2	1	0.5	0.03	--
PATIENT_2	<a href="#">chr10:74928672-75199689</a>	48	2	1	0.5	0.27	--
PATIENT_2	<a href="#">chr10:105152948-105632510</a>	57	2	1	0.5	0.48	--
PATIENT_2	<a href="#">chr16:69279412-69409860</a>	22	2	1.01	0.5	0.13	--

PATIENT_2	<a href="#">chr17:26250531-26350070</a>	18	2	1	0.5	0.1	--
PATIENT_2	<a href="#">chr3:48257686-48576850</a>	91	2	1.01	0.51	0.32	--
PATIENT_2	<a href="#">chr12:8705938-8989363</a>	61	2	1.01	0.51	0.28	--
PATIENT_2	<a href="#">chr17:7199920-7286735</a>	35	2	1.03	0.51	0.09	--
PATIENT_2	<a href="#">chr17:25911810-26155148</a>	10	2	1.01	0.51	0.24	--
PATIENT_2	<a href="#">chr17:68357452-69757105</a>	36	2	1.02	0.51	1.4	--
PATIENT_2	<a href="#">chr1:23995284-23995816</a>	3	2	1.03	0.52	0	--
PATIENT_2	<a href="#">chr3:188932301-188934076</a>	2	2	1.05	0.52	0	<a href="#">BCL6</a>
PATIENT_2	<a href="#">chr10:102722835-104619894</a>	350	2	1.04	0.52	1.9	NFKB2;SUFU;TLX1
PATIENT_2	<a href="#">chr12:129923375-132242894</a>	301	2	1.04	0.52	2.32	<a href="#">ULK1</a>
PATIENT_2	<a href="#">chr15:69234290-69856700</a>	16	2	1.04	0.52	0.62	--
PATIENT_2	<a href="#">chr15:88247533-88603084</a>	30	2	1.05	0.52	0.36	<a href="#">IDH2</a>
PATIENT_2	<a href="#">chr16:69969110-88655961</a>	1095	2	1.05	0.52	18.69	CBFA2T3;CDK10;FANCA;MAF;MLKL
PATIENT_2	<a href="#">chr19:58991009-59069079</a>	10	2	1.03	0.52	0.08	--
PATIENT_2	<a href="#">chr2:136262473-136344345</a>	32	2	1.07	0.53	0.08	--
PATIENT_2	<a href="#">chr3:57969477-58254443</a>	61	2	1.06	0.53	0.28	--
PATIENT_2	<a href="#">chr8:20151833-23355103</a>	281	2	1.07	0.53	3.2	--
PATIENT_2	<a href="#">chr10:101553892-101831260</a>	48	2	1.07	0.53	0.28	--
PATIENT_2	<a href="#">chr10:102039823-102574445</a>	72	2	1.06	0.53	0.53	--
PATIENT_2	<a href="#">chr16:1304065-1762626</a>	164	2	1.05	0.53	0.46	--
PATIENT_2	<a href="#">chr19:1578391-3935240</a>	369	2	1.07	0.53	2.36	CSNK1G2;DAPK3;GNA11;MATK;MKNK2; <a href="#">TCF3</a>
PATIENT_2	<a href="#">chr1:52845074-52936533</a>	8	2	1.08	0.54	0.09	--
PATIENT_2	<a href="#">chr15:71368585-73806695</a>	343	2	1.09	0.54	2.44	CLK3;CSK;PML
PATIENT_2	<a href="#">chr16:45274969-45719860</a>	47	2	1.08	0.54	0.44	--
PATIENT_2	<a href="#">chr16:54166092-57190691</a>	586	2	1.07	0.54	3.02	CSNK2A2;HERPUD1
PATIENT_2	<a href="#">chr12:122304315-129214606</a>	278	2	1.11	0.55	6.91	--
PATIENT_2	<a href="#">chr1:112859128-112864539</a>	4	2	1.12	0.56	0.01	--
PATIENT_2	<a href="#">chr2:120752767-135346594</a>	343	2	1.13	0.56	14.59	<a href="#">ERCC3</a>
PATIENT_2	<a href="#">chr2:171216886-171421827</a>	18	2	1.13	0.56	0.2	<a href="#">MYO3B</a>
PATIENT_2	<a href="#">chr3:58469725-58614494</a>	24	2	1.13	0.56	0.14	--
PATIENT_2	<a href="#">chr8:26283706-27670180</a>	113	2	1.12	0.56	1.39	<a href="#">PTK2B</a>
PATIENT_2	<a href="#">chr12:31008123-31147908</a>	31	2	1.12	0.56	0.14	--

PATIENT_2	<a href="#">chr12:110217557-110379473</a>	28	2	1.13	0.56	0.16	--
PATIENT_2	<a href="#">chr15:66276925-67483110</a>	50	2	1.11	0.56	1.21	--
PATIENT_2	<a href="#">chr16:46290709-49323194</a>	168	2	1.12	0.56	3.03	--
PATIENT_2	<a href="#">chr19:765983-1447367</a>	207	2	1.11	0.56	0.68	--
PATIENT_2	<a href="#">chr10:85926260-88808948</a>	129	2	1.14	0.57	2.88	<a href="#">BMPR1A</a>
PATIENT_2	<a href="#">chr15:63277305-63490585</a>	45	2	1.14	0.57	0.21	--
PATIENT_2	<a href="#">chr2:113974045-114115449</a>	7	2	1.17	0.58	0.14	--
PATIENT_2	<a href="#">chr4:44144485-44145128</a>	3	2	1.17	0.58	0	--
PATIENT_2	<a href="#">chr6:5054689-5376338</a>	5	2	1.16	0.58	0.32	--
PATIENT_2	<a href="#">chr12:51786011-51800885</a>	7	2	1.17	0.58	0.01	--
PATIENT_2	<a href="#">chr13:18646150-18651591</a>	4	2	1.16	0.58	0.01	--
PATIENT_2	<a href="#">chr15:70219337-70624286</a>	73	2	1.16	0.58	0.4	--
PATIENT_2	<a href="#">chr16:52292093-54096803</a>	36	2	1.15	0.58	1.8	--
PATIENT_2	<a href="#">chr17:10384687-10387169</a>	3	2	1.16	0.58	0	--
PATIENT_2	<a href="#">chr4:25273276-25287426</a>	12	2	1.19	0.59	0.01	--
PATIENT_2	<a href="#">chr8:27785437-29258885</a>	83	2	1.18	0.59	1.47	--
PATIENT_2	<a href="#">chr12:46524925-46646208</a>	12	2	1.17	0.59	0.12	--
PATIENT_2	<a href="#">chr12:102902742-102904926</a>	3	2	1.17	0.59	0	--
PATIENT_2	<a href="#">chr12:110581462-110858947</a>	43	2	1.18	0.59	0.28	<a href="#">ALDH2</a>
PATIENT_2	<a href="#">chr14:101546935-101586224</a>	45	2	1.18	0.59	0.04	--
PATIENT_2	<a href="#">chr17:26707664-27349962</a>	56	2	1.18	0.59	0.64	NF1;SUZ12
PATIENT_2	<a href="#">chr10:99193020-99202655</a>	7	2	1.2	0.6	0.01	--
PATIENT_2	<a href="#">chr12:111980509-113278006</a>	144	2	1.21	0.6	1.3	--
PATIENT_2	<a href="#">chr13:109758273-113857355</a>	341	2	1.19	0.6	4.1	--
PATIENT_2	<a href="#">chr16:52061463-52202421</a>	20	2	1.21	0.6	0.14	--
PATIENT_2	<a href="#">chr2:88809940-96055718</a>	82	2	1.22	0.61	7.25	--
PATIENT_2	<a href="#">chr3:48584459-48600779</a>	64	2	1.21	0.61	0.02	--
PATIENT_2	<a href="#">chr4:6343909-6769345</a>	37	2	1.23	0.61	0.43	--
PATIENT_2	<a href="#">chr12:11041276-14839238</a>	196	2	1.23	0.61	3.8	<a href="#">ETV6;GUCY2C</a>
PATIENT_2	<a href="#">chr15:89153431-89276316</a>	59	2	1.22	0.61	0.12	<a href="#">BLM;FES</a>
PATIENT_2	<a href="#">chr1:47375841-47462309</a>	19	2	1.25	0.62	0.09	<a href="#">TAL1</a>
PATIENT_2	<a href="#">chr1:146047476-146483058</a>	12	2	1.24	0.62	0.44	--
PATIENT_2	<a href="#">chr2:118295745-119968533</a>	89	2	1.24	0.62	1.67	--

PATIENT_2	<a href="#">chr2:169705255-170044338</a>	72	2	1.24	0.62	0.34	--
PATIENT_2	<a href="#">chr3:48577318-48582919</a>	21	2	1.24	0.62	0.01	--
PATIENT_2	<a href="#">chr3:52543648-53131517</a>	150	2	1.23	0.62	0.59	NEK4;PBRM1
PATIENT_2	<a href="#">chr15:38975498-39100502</a>	18	2	1.24	0.62	0.13	--
PATIENT_2	<a href="#">chr15:62197432-63213080</a>	114	2	1.25	0.62	1.02	<a href="#">CSNK1G1</a>
PATIENT_2	<a href="#">chr4:40512949-40590111</a>	8	2	1.26	0.63	0.08	--
PATIENT_2	<a href="#">chr14:72474485-72560727</a>	24	2	1.26	0.63	0.09	--
PATIENT_2	<a href="#">chr15:39151440-39897164</a>	134	2	1.26	0.63	0.75	LTK;TYRO3
PATIENT_2	<a href="#">chr17:25001870-25911293</a>	81	2	1.26	0.63	0.91	--
PATIENT_2	<a href="#">chr1:23995985-24009844</a>	10	2	1.27	0.64	0.01	--
PATIENT_2	<a href="#">chr2:69862205-69888586</a>	5	2	1.29	0.64	0.03	--
PATIENT_2	<a href="#">chr3:53504278-53879128</a>	68	2	1.28	0.64	0.37	--
PATIENT_2	<a href="#">chr6:7127228-10904372</a>	151	2	1.27	0.64	3.78	MAK;RIOK1
PATIENT_2	<a href="#">chr7:5220776-5629176</a>	36	2	1.29	0.64	0.41	--
PATIENT_2	<a href="#">chr8:1706898-15552635</a>	280	2	1.28	0.64	13.85	<a href="#">BLK</a>
PATIENT_2	<a href="#">chr10:99108324-99150908</a>	33	2	1.29	0.64	0.04	--
PATIENT_2	<a href="#">chr10:118295617-135223617</a>	872	2	1.29	0.64	16.93	FGFR2;GRK5;STK32C
PATIENT_2	<a href="#">chr12:93489492-93912120</a>	6	2	1.28	0.64	0.42	--
PATIENT_2	<a href="#">chr15:82372990-83289397</a>	62	2	1.28	0.64	0.92	<a href="#">ALPK3</a>
PATIENT_2	<a href="#">chr15:87962415-88150511</a>	68	2	1.28	0.64	0.19	--
PATIENT_2	<a href="#">chr1:113454546-113463522</a>	5	2	1.31	0.65	0.01	--
PATIENT_2	<a href="#">chr1:227633940-227635090</a>	5	2	1.29	0.65	0	--
PATIENT_2	<a href="#">chr4:39921689-40447616</a>	12	2	1.3	0.65	0.53	--
PATIENT_2	<a href="#">chr4:141709270-142108351</a>	7	2	1.31	0.65	0.4	--
PATIENT_2	<a href="#">chr15:38117830-38244617</a>	8	2	1.29	0.65	0.13	<a href="#">BUB1B</a>
PATIENT_2	<a href="#">chr15:84085505-87562863</a>	68	2	1.3	0.65	3.48	<a href="#">NTRK3</a>
PATIENT_2	<a href="#">chr10:105782010-112259970</a>	229	2	1.32	0.66	6.48	--
PATIENT_2	<a href="#">chr11:18692122-18696134</a>	5	2	1.32	0.66	0	--
PATIENT_2	<a href="#">chr12:94601511-94779127</a>	7	2	1.32	0.66	0.18	--
PATIENT_2	<a href="#">chr13:25821263-25876155</a>	11	2	1.33	0.66	0.05	<a href="#">CDK8</a>
PATIENT_2	<a href="#">chr15:73923138-80123560</a>	357	2	1.32	0.66	6.2	--
PATIENT_2	<a href="#">chr16:57309652-60612682</a>	16	2	1.32	0.66	3.3	--
PATIENT_2	<a href="#">chr19:61825202-63774370</a>	213	2	1.31	0.66	1.95	AURKC;TRIM28

PATIENT_2	<a href="#">chr22:34535884-34987650</a>	15	2	1.33	0.66	0.45	--
PATIENT_2	<a href="#">chr8:71130139-71144299</a>	6	2	1.33	0.67	0.01	--
PATIENT_2	<a href="#">chr10:104622269-105150209</a>	54	2	1.34	0.67	0.53	--
PATIENT_2	<a href="#">chr12:8266165-8704743</a>	35	2	1.35	0.67	0.44	--
PATIENT_2	<a href="#">chr14:92477830-92743031</a>	13	2	1.33	0.67	0.27	--
PATIENT_2	<a href="#">chr2:98177321-113915456</a>	769	2	1.35	0.68	15.74	BUB1;MERTK;PAX8;TTL
PATIENT_2	<a href="#">chr8:17201922-20122123</a>	155	2	1.36	0.68	2.92	--
PATIENT_2	<a href="#">chr10:112761468-118020468</a>	331	2	1.36	0.68	5.26	--
PATIENT_2	<a href="#">chr12:29412463-30696441</a>	27	2	1.37	0.68	1.28	--
PATIENT_2	<a href="#">chr12:115456968-117121341</a>	92	2	1.35	0.68	1.66	<a href="#">TAOK3</a>
PATIENT_2	<a href="#">chr12:118394266-119704896</a>	229	2	1.37	0.68	1.31	<a href="#">CIT</a>
PATIENT_2	<a href="#">chr12:129393128-129877727</a>	47	2	1.37	0.68	0.48	--
PATIENT_2	<a href="#">chr13:20447255-20463476</a>	7	2	1.37	0.68	0.02	<a href="#">LATS2</a>
PATIENT_2	<a href="#">chr14:90696442-90994842</a>	14	2	1.35	0.68	0.3	--
PATIENT_2	<a href="#">chr8:23355494-24264728</a>	31	2	1.38	0.69	0.91	--
PATIENT_2	<a href="#">chr12:8167782-8182076</a>	6	2	1.38	0.69	0.01	--
PATIENT_2	<a href="#">chr12:39602410-40253195</a>	28	2	1.39	0.69	0.65	--
PATIENT_2	<a href="#">chr12:62806113-62895867</a>	6	2	1.37	0.69	0.09	--
PATIENT_2	<a href="#">chr12:119911118-122085051</a>	329	2	1.38	0.69	2.17	BCL7A;CAMKK2
PATIENT_2	<a href="#">chr15:87649422-87821819</a>	36	2	1.38	0.69	0.17	--
PATIENT_2	<a href="#">chr10:83625360-85923622</a>	19	2	1.39	0.7	2.3	--
PATIENT_2	<a href="#">chr10:101939359-102038760</a>	41	2	1.4	0.7	0.1	<a href="#">CHUK</a>
PATIENT_2	<a href="#">chr22:35020995-42362371</a>	986	2	1.4	0.7	7.34	CSNK1E;CYP2D6;EP300;MKL1;MYH9; <a href="#">PDGFB</a>

Copy Number Gains in Patient 3							
Sample	Region (hg18)	Number of Exons	Reference Number of Copies	Estimated Copy Number	Copy Number Ratio	Length of Containing Segment	Informative Genes in Region
PATIENT_3	<a href="#">chr3:62360194-62623060</a>	28	2	7.69	3.85	0.26	--
PATIENT_3	<a href="#">chr3:61950426-62331992</a>	37	2	7.55	3.77	0.38	--
PATIENT_3	<a href="#">chr13:24239457-40454150</a>	1158	2	7.02	3.51	16.21	BRCA2;CDK8;CDX2;CSNK1A1L;FLT1; FLT3;LHFP
PATIENT_3	<a href="#">chr8:124860113-124867106</a>	6	2	5.92	2.96	0.01	--

PATIENT_3	<a href="#">chr3:62332316-62333518</a>	5	2	5.47	2.74	0	--
PATIENT_3	<a href="#">chr8:89128047-91713059</a>	83	2	5.1	2.55	2.59	<a href="#">RIPK2</a>
PATIENT_3	<a href="#">chr8:146248682-146250272</a>	6	2	5.06	2.53	0	--
PATIENT_3	<a href="#">chr13:18895240-20340793</a>	167	2	4.95	2.47	1.45	--
PATIENT_3	<a href="#">chr3:62714330-63239388</a>	5	2	4.87	2.44	0.53	--
PATIENT_3	<a href="#">chr8:87129912-88464003</a>	101	2	4.89	2.44	1.33	<a href="#">PSKH2</a>
PATIENT_3	<a href="#">chr13:20518011-24236461</a>	285	2	4.85	2.42	3.72	<a href="#">LATS2</a>
PATIENT_3	<a href="#">chr8:91883088-124859476</a>	1631	2	4.78	2.39	32.98	COX6C;EXT1
PATIENT_3	<a href="#">chr8:124867968-126517580</a>	171	2	4.75	2.37	1.65	<a href="#">TRIB1</a>
PATIENT_3	<a href="#">chr8:71234368-86580208</a>	470	2	4.72	2.36	15.35	--
PATIENT_3	<a href="#">chr3:108912088-110315940</a>	191	2	4.64	2.32	1.4	--
PATIENT_3	<a href="#">chr8:67752530-70836593</a>	221	2	4.36	2.18	3.08	<a href="#">SGK3</a>
PATIENT_3	<a href="#">chr8:67639516-67739506</a>	25	2	4.23	2.12	0.1	--
PATIENT_3	<a href="#">chr8:40508900-67249284</a>	1027	2	4.08	2.04	26.74	CHCHD7;HOOK3;IKBKB;LYN;MOS; PLAG1;POLB
PATIENT_3	<a href="#">chr5:69408132-69769142</a>	7	2	4.07	2.03	0.36	--
PATIENT_3	<a href="#">chr10:51640611-51648330</a>	3	2	4.05	2.03	0.01	--
PATIENT_3	<a href="#">chr20:57849898-57929836</a>	48	2	4.05	2.03	0.08	--
PATIENT_3	<a href="#">chr8:128497824-146142308</a>	1554	2	3.99	2	17.64	ADCK5;MAPK15;MYC;NRBP2;PTK2
PATIENT_3	<a href="#">chr13:18221912-18653904</a>	9	2	3.96	1.98	0.43	--
PATIENT_3	<a href="#">chr3:151046528-151168918</a>	13	2	3.92	1.96	0.12	--
PATIENT_3	<a href="#">chr8:71188432-71231961</a>	19	2	3.92	1.96	0.04	--
PATIENT_3	<a href="#">chr3:157653392-158800836</a>	78	2	3.87	1.94	1.15	--
PATIENT_3	<a href="#">chr7:142788818-142788958</a>	2	2	3.81	1.91	0	--
PATIENT_3	<a href="#">chr3:108579234-108580022</a>	5	2	3.77	1.89	0	--
PATIENT_3	<a href="#">chr8:88954222-89122960</a>	5	2	3.63	1.82	0.17	--
PATIENT_3	<a href="#">chr13:20374842-20463470</a>	19	2	3.6	1.8	0.09	<a href="#">LATS2</a>
PATIENT_3	<a href="#">chr20:57200078-57200453</a>	3	2	3.58	1.79	0	--
PATIENT_3	<a href="#">chr7:7240578-28825346</a>	958	2	3.51	1.76	21.58	HNRNPA2B1;HOXA11;HOXA13;HOXA9;JAZF1; <a href="#">STK31</a>
PATIENT_3	<a href="#">chr7:29001956-30454466</a>	78	2	3.52	1.76	1.45	--

PATIENT_3	<a href="#">chr3:110319557-110695659</a>	23	2	3.43	1.72	0.38	--
PATIENT_3	<a href="#">chr13:40533798-40554968</a>	12	2	3.43	1.72	0.02	--
PATIENT_3	<a href="#">chr13:46122392-48679369</a>	144	2	3.42	1.71	2.56	<a href="#">RB1</a>
PATIENT_3	<a href="#">chr13:40689297-44454218</a>	231	2	3.39	1.7	3.76	--
PATIENT_3	<a href="#">chr3:63404160-63950978</a>	24	2	3.38	1.69	0.55	--
PATIENT_3	<a href="#">chr7:53071656-55466450</a>	48	2	3.35	1.67	2.39	<a href="#">EGFR</a>
PATIENT_3	<a href="#">chr13:45323688-45844087</a>	70	2	3.34	1.67	0.52	<a href="#">LCP1</a>
PATIENT_3	<a href="#">chr8:67739709-67741618</a>	10	2	3.32	1.66	0	--
PATIENT_3	<a href="#">chr8:126517844-128497353</a>	6	2	3.32	1.66	1.98	<a href="#">TRIB1</a>
PATIENT_3	<a href="#">chr10:47429216-47468794</a>	14	2	3.28	1.64	0.04	--
PATIENT_3	<a href="#">chr7:30461353-51255000</a>	1352	2	3.24	1.62	20.79	CAMK2B;STK17A
PATIENT_3	<a href="#">chr13:44461818-45174940</a>	79	2	3.22	1.61	0.71	--
PATIENT_3	<a href="#">chr13:48693276-51849918</a>	280	2	3.19	1.6	3.16	<a href="#">NEK5</a>
PATIENT_3	<a href="#">chr20:56660511-57051149</a>	81	2	3.21	1.6	0.39	<a href="#">GNAS</a>
PATIENT_3	<a href="#">chr20:57202305-57848865</a>	26	2	3.21	1.6	0.65	--
PATIENT_3	<a href="#">chr13:72201146-114109832</a>	1743	2	3.17	1.59	41.91	ERCC5;STK24
PATIENT_3	<a href="#">chr21:9928833-9995590</a>	23	2	3.18	1.59	0.07	--
PATIENT_3	<a href="#">chr8:67504712-67590745</a>	23	2	3.16	1.58	0.09	--
PATIENT_3	<a href="#">chr13:51874698-72191144</a>	204	2	3.15	1.57	20.32	--
PATIENT_3	<a href="#">chr6:57133858-57298727</a>	17	2	3.11	1.56	0.16	--
PATIENT_3	<a href="#">chr3:151171256-152173062</a>	66	2	3.09	1.55	1	--
PATIENT_3	<a href="#">chr3:153500760-157622116</a>	176	2	3.1	1.55	4.12	--
PATIENT_3	<a href="#">chr20:47301498-56452614</a>	528	2	3.11	1.55	9.15	<a href="#">AURKA</a>
PATIENT_3	<a href="#">chr11:66149267-66149408</a>	2	2	3.08	1.54	0	--
PATIENT_3	<a href="#">chr8:70906617-71144602</a>	18	2	3.06	1.53	0.24	--
PATIENT_3	<a href="#">chr1:154318306-154318394</a>	2	2	3.05	1.52	0	--
PATIENT_3	<a href="#">chr3:190066760-195874124</a>	308	2	3.04	1.52	5.81	<a href="#">LPP</a>
PATIENT_3	<a href="#">chr20:16382-818924</a>	112	2	3.05	1.52	0.8	CSNK2A1;TRIB3
PATIENT_3	<a href="#">chr20:38750653-47298000</a>	1100	2	3.04	1.52	8.55	ADA;MAFB;SGK2;STK4;TOP1; <a href="#">TP53RK</a>
PATIENT_3	<a href="#">chr8:35521546-35767522</a>	19	2	3.02	1.51	0.25	--
PATIENT_3	<a href="#">chr10:11567862-11679626</a>	11	2	3.01	1.51	0.11	--

PATIENT_3	<a href="#">chr8:91726694-91873332</a>	3	2	2.97	1.48	0.15	--
PATIENT_3	<a href="#">chr4:14619100-14663202</a>	4	2	2.92	1.46	0.04	--
PATIENT_3	<a href="#">chr20:1112431-1183009</a>	18	2	2.92	1.46	0.07	--
PATIENT_3	<a href="#">chr12:55788264-55809040</a>	2	2	2.91	1.45	0.02	--
PATIENT_3	<a href="#">chr10:49279752-49309280</a>	11	2	2.89	1.44	0.03	<a href="#">MAPK8</a>
PATIENT_3	<a href="#">chr16:69770381-69877183</a>	13	2	2.89	1.44	0.11	--
PATIENT_3	<a href="#">chr2:84487115-84899992</a>	105	2	2.86	1.43	0.41	--
PATIENT_3	<a href="#">chr3:144753922-148589320</a>	79	2	2.85	1.43	3.84	--
PATIENT_3	<a href="#">chr20:57930816-62375296</a>	802	2	2.86	1.43	4.44	PTK6;SRMS;SS18L1
PATIENT_3	<a href="#">chr5:40752174-40870428</a>	21	2	2.84	1.42	0.12	<a href="#">PRKAA1</a>
PATIENT_3	<a href="#">chr1:159826072-159867468</a>	9	2	2.82	1.41	0.04	--
PATIENT_3	<a href="#">chr3:184020800-184166132</a>	35	2	2.82	1.41	0.15	--
PATIENT_3	<a href="#">chr3:197000840-199381079</a>	327	2	2.81	1.41	2.38	PAK2;TFRC;TNK2
PATIENT_3	<a href="#">chr3:140545632-140584892</a>	29	2	2.8	1.4	0.04	--
PATIENT_3	<a href="#">chr5:180307954-180362342</a>	11	2	2.8	1.4	0.05	--
PATIENT_3	<a href="#">chr20:5970858-38750053</a>	2494	2	2.79	1.4	32.78	ASXL1;HCK;MAFB;MYLK2;PAK7; <a href="#">SRC</a>
PATIENT_3	<a href="#">chr3:161459045-166388412</a>	164	2	2.78	1.39	4.93	--
PATIENT_3	<a href="#">chr5:32171480-39430130</a>	708	2	2.78	1.39	7.26	<a href="#">LIFR</a>
PATIENT_3	<a href="#">chr7:117219688-119701954</a>	21	2	2.77	1.38	2.48	--
PATIENT_3	<a href="#">chr1:196468356-196514750</a>	6	2	2.74	1.37	0.05	<a href="#">NEK7</a>
PATIENT_3	<a href="#">chr7:290704-6830832</a>	851	2	2.75	1.37	6.54	CARD11;EIF2AK1;PMS2
PATIENT_3	<a href="#">chr16:79132468-79632514</a>	28	2	2.75	1.37	0.5	--
PATIENT_3	<a href="#">chrX:43400564-44287006</a>	56	1	1.37	1.37	0.89	--
PATIENT_3	<a href="#">chr3:63951512-63980078</a>	14	2	2.72	1.36	0.03	--
PATIENT_3	<a href="#">chr5:40964464-45681260</a>	255	2	2.72	1.36	4.72	<a href="#">MGC42105</a>
PATIENT_3	<a href="#">chr3:159298651-161195944</a>	91	2	2.71	1.35	1.9	<a href="#">MLF1</a>
PATIENT_3	<a href="#">chr3:196298999-196986736</a>	98	2	2.69	1.35	0.69	--
PATIENT_3	<a href="#">chrX:109583997-110911909</a>	104	1	1.35	1.35	1.33	<a href="#">PAK3</a>
PATIENT_3	<a href="#">chr2:182465122-198248337</a>	989	2	2.67	1.34	15.78	PMS1;STK17B
PATIENT_3	<a href="#">chr3:148613066-150992792</a>	146	2	2.68	1.34	2.38	--
PATIENT_3	<a href="#">chr5:6544384-31588672</a>	589	2	2.67	1.34	25.04	<a href="#">TRIO</a>
PATIENT_3	<a href="#">chr7:114350764-117218424</a>	153	2	2.69	1.34	2.87	<a href="#">MET</a>

PATIENT_3	<a href="#">chrX:111910861-114330622</a>	63	1	1.34	1.34	2.42	--
PATIENT_3	<a href="#">chr3:72510335-86198562</a>	199	2	2.67	1.33	13.69	--
PATIENT_3	<a href="#">chr3:113120670-115697496</a>	411	2	2.66	1.33	2.58	--
PATIENT_3	<a href="#">chr7:55508133-69865889</a>	312	2	2.65	1.32	14.36	PHKG1;SBDS
PATIENT_3	<a href="#">chr11:1220816-1221476</a>	4	2	2.65	1.32	0	--
PATIENT_3	<a href="#">chr1:233973983-233985470</a>	7	2	2.62	1.31	0.01	--
PATIENT_3	<a href="#">chr3:89611298-107069002</a>	549	2	2.62	1.31	17.46	CBLB;EPHA3;TFG
PATIENT_3	<a href="#">chr7:30457473-30459064</a>	8	2	2.63	1.31	0	--
PATIENT_3	<a href="#">chr7:99083908-99311654</a>	54	2	2.63	1.31	0.23	--
PATIENT_3	<a href="#">chr20:57200656-57202048</a>	9	2	2.61	1.31	0	--
PATIENT_3	<a href="#">chrX:107150617-109471128</a>	230	1	1.31	1.31	2.32	<a href="#">GUCY2F</a>
PATIENT_3	<a href="#">chr2:137589224-163403217</a>	1188	2	2.61	1.3	25.81	ACVR1;ACVR1C;ACVR2A
PATIENT_3	<a href="#">chr2:164299660-174908871</a>	998	2	2.61	1.3	10.61	MYO3B;PDK1;STK39;TLK1;ZAK
PATIENT_3	<a href="#">chr7:76093281-90585362</a>	733	2	2.6	1.3	14.49	--
PATIENT_3	<a href="#">chr17:44010578-44045830</a>	13	2	2.6	1.3	0.04	--

Copy Number Losses in Patient 3							
Sample	Region (hg18)	Number of Exons	Reference Number of Copies	Estimated Copy Number	Copy Number Ratio	Length of Containing Segment	Informative Genes in Region
PATIENT_3	<a href="#">chr5:175449982-175452847</a>	2	2	0.54	0.27	0	--
PATIENT_3	<a href="#">chr11:89341468-89346505</a>	5	2	0.75	0.37	0.01	--
PATIENT_3	<a href="#">chr11:4932642-4933152</a>	3	2	0.76	0.38	0	--
PATIENT_3	<a href="#">chr15:28451713-28452491</a>	2	2	0.8	0.4	0	--
PATIENT_3	<a href="#">chr5:140553928-140554363</a>	3	2	0.82	0.41	0	--
PATIENT_3	<a href="#">chr8:8692343-8786385</a>	7	2	0.84	0.42	0.09	--
PATIENT_3	<a href="#">chr10:104995884-105038399</a>	11	2	0.86	0.43	0.04	--
PATIENT_3	<a href="#">chr21:46247784-46248032</a>	2	2	0.93	0.47	0	--
PATIENT_3	<a href="#">chr18:42797654-42809168</a>	4	2	0.97	0.48	0.01	--
PATIENT_3	<a href="#">chr19:11194428-11194716</a>	3	2	0.96	0.48	0	--
PATIENT_3	<a href="#">chr6:99428968-99460254</a>	6	2	0.97	0.49	0.03	--
PATIENT_3	<a href="#">chr5:140534638-140539396</a>	10	2	1	0.5	0	--
PATIENT_3	<a href="#">chr14:23850015-23850237</a>	2	2	0.99	0.5	0	--
PATIENT_3	<a href="#">chr10:134849676-134849836</a>	2	2	1.01	0.51	0	--
PATIENT_3	<a href="#">chr8:180898-8680949</a>	299	2	1.1	0.55	8.5	--
PATIENT_3	<a href="#">chr8:10507783-29263472</a>	1443	2	1.1	0.55	18.76	BLK;PBK;PTK2B

PATIENT_3	<a href="#">chr8:30051028-33574460</a>	224	2	1.1	0.55	3.52	<a href="#">WRN</a>
PATIENT_3	<a href="#">chr1:110032028-110037400</a>	8	2	1.12	0.56	0.01	--
PATIENT_3	<a href="#">chr8:8786572-10505640</a>	80	2	1.12	0.56	1.72	--
PATIENT_3	<a href="#">chr6:137285281-137287296</a>	5	2	1.15	0.57	0	--
PATIENT_3	<a href="#">chr6:150046326-150047098</a>	5	2	1.15	0.57	0	<a href="#">LATS1</a>
PATIENT_3	<a href="#">chr15:18429928-19073754</a>	16	2	1.14	0.57	0.64	--
PATIENT_3	<a href="#">chr16:30523396-30523728</a>	3	2	1.14	0.57	0	--
PATIENT_3	<a href="#">chr18:28603672-28604242</a>	4	2	1.14	0.57	0	--
PATIENT_3	<a href="#">chrX:48303336-48303516</a>	2	1	0.57	0.57	0	--
PATIENT_3	<a href="#">chr15:19331323-19991357</a>	23	2	1.17	0.58	0.66	--
PATIENT_3	<a href="#">chr18:46444442-46506424</a>	5	2	1.16	0.58	0.06	<a href="#">MAPK4</a>
PATIENT_3	<a href="#">chr11:76978766-76979086</a>	3	2	1.18	0.59	0	--
PATIENT_3	<a href="#">chr17:24109851-24110377</a>	3	2	1.18	0.59	0	--
PATIENT_3	<a href="#">chr4:147780572-147781162</a>	4	2	1.2	0.6	0	--
PATIENT_3	<a href="#">chr1:90950443-90950611</a>	2	2	1.22	0.61	0	--
PATIENT_3	<a href="#">chr1:154502396-154502728</a>	3	2	1.21	0.61	0	--
PATIENT_3	<a href="#">chr4:171149094-171149754</a>	3	2	1.22	0.61	0	--
PATIENT_3	<a href="#">chr18:58005838-58006166</a>	3	2	1.23	0.61	0	--
PATIENT_3	<a href="#">chr19:8456480-8456873</a>	3	2	1.22	0.61	0	--
PATIENT_3	<a href="#">chr4:140183804-140200122</a>	8	2	1.23	0.62	0.02	--
PATIENT_3	<a href="#">chr4:189161851-189305469</a>	19	2	1.23	0.62	0.14	--
PATIENT_3	<a href="#">chr6:101002793-101004228</a>	5	2	1.25	0.62	0	--
PATIENT_3	<a href="#">chr6:144304308-144305044</a>	5	2	1.23	0.62	0	--
PATIENT_3	<a href="#">chr9:33912560-33913831</a>	7	2	1.24	0.62	0	--
PATIENT_3	<a href="#">chr2:233058924-233059249</a>	3	2	1.26	0.63	0	--
PATIENT_3	<a href="#">chr4:123073014-123073534</a>	4	2	1.26	0.63	0	--
PATIENT_3	<a href="#">chr5:78568809-78569218</a>	3	2	1.27	0.63	0	--
PATIENT_3	<a href="#">chr9:71320776-71321768</a>	7	2	1.25	0.63	0	--
PATIENT_3	<a href="#">chr1:195010654-195067638</a>	11	2	1.3	0.65	0.06	--
PATIENT_3	<a href="#">chr5:175327706-175444580</a>	2	2	1.3	0.65	0.12	--
PATIENT_3	<a href="#">chr16:27367900-27380348</a>	3	2	1.3	0.65	0.01	<a href="#">IL21R</a>
PATIENT_3	<a href="#">chr2:42524992-42573985</a>	4	2	1.32	0.66	0.05	--
PATIENT_3	<a href="#">chr3:185583202-185584056</a>	6	2	1.32	0.66	0	--

PATIENT_3	<a href="#">chr22:39975340-40315696</a>	93	2	1.31	0.66	0.34	--
PATIENT_3	<a href="#">chr5:68751262-68752052</a>	6	2	1.35	0.67	0	--
PATIENT_3	<a href="#">chr5:141674108-141674536</a>	3	2	1.34	0.67	0	--
PATIENT_3	<a href="#">chr6:138793717-138796289</a>	14	2	1.34	0.67	0	--
PATIENT_3	<a href="#">chr9:96102276-96128014</a>	16	2	1.35	0.67	0.03	--
PATIENT_3	<a href="#">chr6:71722388-71722785</a>	3	2	1.36	0.68	0	--
PATIENT_3	<a href="#">chr8:86761052-86761766</a>	2	2	1.36	0.68	0	--
PATIENT_3	<a href="#">chr10:112827910-112828869</a>	4	2	1.36	0.68	0	--
PATIENT_3	<a href="#">chr15:50868306-50869309</a>	7	2	1.35	0.68	0	--
PATIENT_3	<a href="#">chr19:41365329-41366402</a>	7	2	1.36	0.68	0	--
PATIENT_3	<a href="#">chr5:137831144-137831556</a>	3	2	1.39	0.69	0	--
PATIENT_3	<a href="#">chr1:211098552-211098934</a>	4	2	1.39	0.7	0	--
PATIENT_3	<a href="#">chr2:204013985-204014143</a>	2	2	1.4	0.7	0	--
PATIENT_3	<a href="#">chr4:191140678-191185332</a>	16	2	1.4	0.7	0.04	--
PATIENT_3	<a href="#">chr6:32579834-32742301</a>	22	2	1.39	0.7	0.16	--

Sample	Region (hg18)	Copy Number Gains in Patient 4						Informative Genes in Region
		Number of Exons	Reference Number of Copies	Estimated Copy Number	Copy Number Ratio	Length of Containing Segment		
PATIENT_4	<a href="#">chr4:42219000-42323818</a>	22	2	6.16	3.08	0.1	--	
PATIENT_4	<a href="#">chr20:62361942-62375296</a>	6	2	5.95	2.98	0.01	--	
PATIENT_4	<a href="#">chr11:49124970-49184239</a>	18	2	5.7	2.85	0.06	--	
PATIENT_4	<a href="#">chr15:100279908-100280208</a>	3	2	5.7	2.85	0	--	
PATIENT_4	<a href="#">chr20:57844979-57930816</a>	51	2	5.69	2.84	0.09	--	
PATIENT_4	<a href="#">chr11:27999358-28308558</a>	24	2	5.21	2.61	0.31	--	
PATIENT_4	<a href="#">chr17:66357999-67629211</a>	40	2	5.13	2.56	1.27	--	
PATIENT_4	<a href="#">chr17:63952263-64822092</a>	222	2	4.93	2.47	0.87	<a href="#">PRKAR1A</a>	
PATIENT_4	<a href="#">chr4:42109728-42203890</a>	15	2	4.87	2.44	0.09	--	
PATIENT_4	<a href="#">chr11:11862634-11934207</a>	28	2	4.69	2.35	0.07	--	
PATIENT_4	<a href="#">chr11:22663835-26690794</a>	71	2	4.58	2.29	4.03	--	
PATIENT_4	<a href="#">chr11:30309116-31768116</a>	83	2	4.55	2.28	1.46	--	
PATIENT_4	<a href="#">chr11:14750084-14856329</a>	16	2	4.45	2.23	0.11	--	
PATIENT_4	<a href="#">chr11:20761820-22354700</a>	54	2	4.44	2.22	1.59	--	

PATIENT_4	<a href="#">chr20:55340334-55382152</a>	21	2	4.43	2.21	0.04	--
PATIENT_4	<a href="#">chr2:154705175-155015231</a>	10	2	4.36	2.18	0.31	--
PATIENT_4	<a href="#">chr3:164055326-166276422</a>	52	2	4.36	2.18	2.22	--
PATIENT_4	<a href="#">chr5:122951702-122977967</a>	8	2	4.35	2.18	0.03	<a href="#">CSNK1G3</a>
PATIENT_4	<a href="#">chr11:15218600-16733107</a>	25	2	4.37	2.18	1.51	--
PATIENT_4	<a href="#">chr17:62504938-62771350</a>	39	2	4.36	2.18	0.27	--
PATIENT_4	<a href="#">chr20:57782822-57814562</a>	2	2	4.36	2.18	0.03	--
PATIENT_4	<a href="#">chr8:79750612-79872926</a>	13	2	4.33	2.17	0.12	--
PATIENT_4	<a href="#">chr20:57947585-58079200</a>	28	2	4.34	2.17	0.13	--
PATIENT_4	<a href="#">chr4:115968464-116117829</a>	13	2	4.3	2.15	0.15	--
PATIENT_4	<a href="#">chr11:34635042-35243771</a>	44	2	4.29	2.15	0.61	--
PATIENT_4	<a href="#">chr4:126604230-126628022</a>	7	2	4.27	2.14	0.02	--
PATIENT_4	<a href="#">chr1:217419150-217642509</a>	5	2	4.27	2.13	0.22	--
PATIENT_4	<a href="#">chr2:187919280-189677258</a>	142	2	4.25	2.13	1.76	--
PATIENT_4	<a href="#">chr11:49186474-49960474</a>	11	2	4.21	2.11	0.77	--
PATIENT_4	<a href="#">chr2:207738476-207842282</a>	2	2	4.19	2.1	0.1	--
PATIENT_4	<a href="#">chr6:128176546-128427588</a>	25	2	4.2	2.1	0.25	--
PATIENT_4	<a href="#">chr11:48284426-48284690</a>	3	2	4.19	2.1	0	--
PATIENT_4	<a href="#">chr1:247174693-247179172</a>	11	2	4.17	2.09	0	--
PATIENT_4	<a href="#">chr2:162419809-163401478</a>	124	2	4.17	2.09	0.98	--
PATIENT_4	<a href="#">chr8:116700942-116705011</a>	5	2	4.19	2.09	0	--
PATIENT_4	<a href="#">chr4:81047630-81211796</a>	16	2	4.17	2.08	0.16	--
PATIENT_4	<a href="#">chr11:27035373-27479676</a>	40	2	4.15	2.08	0.44	--
PATIENT_4	<a href="#">chrX:31436252-32542414</a>	48	2	4.14	2.07	1.11	--
PATIENT_4	<a href="#">chr20:26009919-28203360</a>	8	2	4.11	2.06	2.19	--
PATIENT_4	<a href="#">chr8:62637914-62764772</a>	24	2	4.09	2.04	0.13	--
PATIENT_4	<a href="#">chr5:49999670-50125859</a>	11	2	4.07	2.03	0.13	--
PATIENT_4	<a href="#">chr8:73097784-73146570</a>	27	2	4.06	2.03	0.05	--
PATIENT_4	<a href="#">chr17:49256948-50697887</a>	49	2	4.07	2.03	1.44	<a href="#">HLF</a>
PATIENT_4	<a href="#">chr21:46843772-46908644</a>	11	2	4.07	2.03	0.06	--
PATIENT_4	<a href="#">chr6:91283038-96160470</a>	43	2	4.03	2.02	4.88	<a href="#">EPHA7;MAP3K7</a>
PATIENT_4	<a href="#">chr20:51994906-54009236</a>	46	2	4.05	2.02	2.01	--

PATIENT_4	<a href="#">chr1:212245169-212521290</a>	4	2	4.02	2.01	0.28	--
PATIENT_4	<a href="#">chr5:108745270-110120320</a>	44	2	4.02	2.01	1.38	--
PATIENT_4	<a href="#">chr20:39091502-39221725</a>	22	2	4.03	2.01	0.13	<a href="#">TOP1</a>
PATIENT_4	<a href="#">chr20:39467431-40947914</a>	83	2	4.01	2	1.48	--
PATIENT_4	<a href="#">chr2:56456500-58321876</a>	31	2	3.99	1.99	1.87	<a href="#">VRK2</a>
PATIENT_4	<a href="#">chr3:101953152-102104177</a>	32	2	3.97	1.99	0.15	--
PATIENT_4	<a href="#">chr3:147271257-148589320</a>	50	2	3.98	1.99	1.32	--
PATIENT_4	<a href="#">chr15:30967710-31144498</a>	12	2	3.99	1.99	0.18	--
PATIENT_4	<a href="#">chr11:20367913-20472086</a>	12	2	3.95	1.98	0.1	--
PATIENT_4	<a href="#">chrX:115483072-115507051</a>	14	2	3.96	1.98	0.02	--
PATIENT_4	<a href="#">chr3:98427884-99148926</a>	52	2	3.95	1.97	0.72	--
PATIENT_4	<a href="#">chr7:37856418-37903099</a>	15	2	3.94	1.97	0.05	--
PATIENT_4	<a href="#">chr11:8370616-8451328</a>	12	2	3.93	1.97	0.08	<a href="#">STK33</a>
PATIENT_4	<a href="#">chr20:36555079-36636904</a>	29	2	3.94	1.97	0.08	--
PATIENT_4	<a href="#">chr20:43185946-43339708</a>	28	2	3.94	1.97	0.15	--
PATIENT_4	<a href="#">chrX:21354632-21580494</a>	25	2	3.94	1.97	0.23	--
PATIENT_4	<a href="#">chr5:50128615-50716270</a>	17	2	3.91	1.96	0.59	--
PATIENT_4	<a href="#">chr6:64752282-70127530</a>	77	2	3.93	1.96	5.38	--
PATIENT_4	<a href="#">chr11:33720068-33748900</a>	10	2	3.93	1.96	0.03	--
PATIENT_4	<a href="#">chr17:51199747-52026727</a>	26	2	3.92	1.96	0.83	--
PATIENT_4	<a href="#">chr2:176869854-177683933</a>	11	2	3.9	1.95	0.81	--
PATIENT_4	<a href="#">chr6:101004902-102622986</a>	69	2	3.89	1.95	1.62	--
PATIENT_4	<a href="#">chr8:65671840-65699572</a>	8	2	3.9	1.95	0.03	--
PATIENT_4	<a href="#">chr1:161305856-161592224</a>	29	2	3.87	1.94	0.29	--
PATIENT_4	<a href="#">chr11:12989159-14113615</a>	45	2	3.87	1.93	1.12	--
PATIENT_4	<a href="#">chr11:17759820-18081404</a>	35	2	3.86	1.93	0.32	--
PATIENT_4	<a href="#">chr3:115581839-116865375</a>	12	2	3.84	1.92	1.28	--
PATIENT_4	<a href="#">chr3:166390862-170581987</a>	113	2	3.84	1.92	4.19	--
PATIENT_4	<a href="#">chr6:97077806-97170270</a>	23	2	3.84	1.92	0.09	--
PATIENT_4	<a href="#">chr7:14700286-16412358</a>	35	2	3.84	1.92	1.71	--
PATIENT_4	<a href="#">chr3:142158156-142175424</a>	6	2	3.81	1.91	0.02	--
PATIENT_4	<a href="#">chr4:142363002-143571812</a>	45	2	3.83	1.91	1.21	--

PATIENT_4	<a href="#">chr4:162595660-164466008</a>	25	2	3.82	1.91	1.87	--
PATIENT_4	<a href="#">chr7:92603175-94097029</a>	153	2	3.82	1.91	1.49	--
PATIENT_4	<a href="#">chr9:74505304-74974795</a>	42	2	3.81	1.91	0.47	--
PATIENT_4	<a href="#">chr11:19121151-19870626</a>	48	2	3.82	1.91	0.75	--
PATIENT_4	<a href="#">chr6:135767780-135826070</a>	15	2	3.79	1.9	0.06	--
PATIENT_4	<a href="#">chr18:9107879-9271118</a>	41	2	3.8	1.9	0.16	--
PATIENT_4	<a href="#">chr5:160685999-161511330</a>	39	2	3.78	1.89	0.83	--
PATIENT_4	<a href="#">chr6:53814926-56551636</a>	185	2	3.79	1.89	2.74	--
PATIENT_4	<a href="#">chr8:68698990-69893022</a>	58	2	3.76	1.88	1.19	--
PATIENT_4	<a href="#">chr11:6870194-7774123</a>	120	2	3.77	1.88	0.9	--
PATIENT_4	<a href="#">chr4:144761678-144833758</a>	4	2	3.74	1.87	0.07	--
PATIENT_4	<a href="#">chr4:144919858-146249776</a>	38	2	3.73	1.87	1.33	--
PATIENT_4	<a href="#">chr5:52180996-52440154</a>	65	2	3.73	1.87	0.26	--
PATIENT_4	<a href="#">chr8:72285990-72431248</a>	16	2	3.73	1.87	0.15	--
PATIENT_4	<a href="#">chr15:92658561-94670541</a>	23	2	3.74	1.87	2.01	--
PATIENT_4	<a href="#">chr6:70139058-71041162</a>	99	2	3.72	1.86	0.9	--
PATIENT_4	<a href="#">chr15:51597206-53270494</a>	76	2	3.72	1.86	1.67	--
PATIENT_4	<a href="#">chr21:18554424-25898092</a>	60	2	3.71	1.86	7.34	--
PATIENT_4	<a href="#">chr1:183542814-197169026</a>	673	2	3.7	1.85	13.63	NEK7;PTGS2;TPR
PATIENT_4	<a href="#">chr2:136592070-148449968</a>	236	2	3.7	1.85	11.86	<a href="#">ACVR2A</a>
PATIENT_4	<a href="#">chr6:47762715-47789644</a>	7	2	3.71	1.85	0.03	--
PATIENT_4	<a href="#">chr17:46698584-47590106</a>	20	2	3.7	1.85	0.89	--
PATIENT_4	<a href="#">chr4:152899458-153522861</a>	14	2	3.67	1.84	0.62	<a href="#">FBXW7</a>
PATIENT_4	<a href="#">chr6:47579032-47755866</a>	21	2	3.68	1.84	0.18	--
PATIENT_4	<a href="#">chr6:122775262-127558778</a>	174	2	3.67	1.84	4.78	--
PATIENT_4	<a href="#">chr17:64922724-65683888</a>	23	2	3.68	1.84	0.76	<a href="#">MAP2K6</a>
PATIENT_4	<a href="#">chrX:83002830-83582212</a>	47	2	3.68	1.84	0.58	<a href="#">RPS6KA6</a>
PATIENT_4	<a href="#">chrX:85518494-86811012</a>	26	2	3.68	1.84	1.29	--
PATIENT_4	<a href="#">chr1:165093483-165105336</a>	6	2	3.65	1.83	0.01	--
PATIENT_4	<a href="#">chr4:147323556-147662260</a>	15	2	3.67	1.83	0.34	--
PATIENT_4	<a href="#">chr5:115346958-115656090</a>	26	2	3.65	1.83	0.31	--
PATIENT_4	<a href="#">chr6:79968118-81039623</a>	60	2	3.67	1.83	1.07	<a href="#">TTK</a>
PATIENT_4	<a href="#">chr6:127940148-128176242</a>	12	2	3.65	1.83	0.24	--

PATIENT_4	<a href="#">chr6:142529096-142806252</a>	38	2	3.67	1.83	0.28	--
PATIENT_4	<a href="#">chr7:16782432-17903530</a>	60	2	3.67	1.83	1.12	--
PATIENT_4	<a href="#">chr17:71553026-71578070</a>	15	2	3.66	1.83	0.03	--
PATIENT_4	<a href="#">chr21:27755492-29176388</a>	15	2	3.66	1.83	1.42	--
PATIENT_4	<a href="#">chr4:110009741-110441218</a>	18	2	3.64	1.82	0.43	--
PATIENT_4	<a href="#">chr4:166633806-169606428</a>	117	2	3.65	1.82	2.97	--
PATIENT_4	<a href="#">chr5:66515974-67629078</a>	21	2	3.63	1.82	1.11	<a href="#">PIK3R1</a>
PATIENT_4	<a href="#">chr7:18133404-19002179</a>	26	2	3.65	1.82	0.87	--
PATIENT_4	<a href="#">chr20:37031194-38750053</a>	23	2	3.64	1.82	1.72	<a href="#">MAFB</a>
PATIENT_4	<a href="#">chr20:62300679-62342174</a>	25	2	3.64	1.82	0.04	--
PATIENT_4	<a href="#">chrX:78314036-78505636</a>	6	2	3.64	1.82	0.19	--
PATIENT_4	<a href="#">chr2:237660550-237906880</a>	10	2	3.63	1.81	0.25	--
PATIENT_4	<a href="#">chr4:74226363-74827041</a>	75	2	3.63	1.81	0.6	--
PATIENT_4	<a href="#">chr4:90866817-94912460</a>	60	2	3.63	1.81	4.05	--
PATIENT_4	<a href="#">chr6:99428968-99481108</a>	9	2	3.62	1.81	0.05	--
PATIENT_4	<a href="#">chr6:143821969-143865288</a>	15	2	3.62	1.81	0.04	--
PATIENT_4	<a href="#">chr9:117202522-117989308</a>	26	2	3.61	1.81	0.79	--
PATIENT_4	<a href="#">chr15:19305362-19331064</a>	13	2	3.61	1.81	0.03	--
PATIENT_4	<a href="#">chr20:48953882-49008404</a>	10	2	3.61	1.81	0.05	--
PATIENT_4	<a href="#">chr2:178689289-182176978</a>	883	2	3.6	1.8	3.49	<a href="#">TTN</a>
PATIENT_4	<a href="#">chr3:144422639-145033624</a>	31	2	3.6	1.8	0.61	--
PATIENT_4	<a href="#">chr4:75259178-75914336</a>	30	2	3.6	1.8	0.66	--
PATIENT_4	<a href="#">chr4:164647670-165338284</a>	17	2	3.6	1.8	0.69	--
PATIENT_4	<a href="#">chr5:41185818-42753937</a>	60	2	3.6	1.8	1.57	--
PATIENT_4	<a href="#">chr5:115836672-118308174</a>	23	2	3.6	1.8	2.47	--
PATIENT_4	<a href="#">chr7:117219688-117667224</a>	20	2	3.6	1.8	0.45	--
PATIENT_4	<a href="#">chr8:124859476-124894020</a>	21	2	3.61	1.8	0.03	--
PATIENT_4	<a href="#">chr11:135259051-35503660</a>	23	2	3.61	1.8	0.24	--
PATIENT_4	<a href="#">chr15:37673865-37859674</a>	25	2	3.6	1.8	0.19	--
PATIENT_4	<a href="#">chr22:49523573-49563256</a>	11	2	3.6	1.8	0.04	--
PATIENT_4	<a href="#">chr3:103060868-110315940</a>	246	2	3.57	1.79	7.26	<a href="#">CBLB</a>
PATIENT_4	<a href="#">chr4:106510336-108841817</a>	102	2	3.58	1.79	2.33	--

PATIENT_4	<a href="#">chr6:163069306-165995448</a>	50	2	3.58	1.79	2.93	--
PATIENT_4	<a href="#">chr7:49922258-50426979</a>	27	2	3.58	1.79	0.5	--
PATIENT_4	<a href="#">chr20:54374558-54404130</a>	13	2	3.59	1.79	0.03	<a href="#">AURKA</a>
PATIENT_4	<a href="#">chr21:27218739-27248987</a>	8	2	3.58	1.79	0.03	--
PATIENT_4	<a href="#">chrX:100865068-100867136</a>	6	2	3.58	1.79	0	--
PATIENT_4	<a href="#">chr1:165227287-165257608</a>	10	2	3.57	1.78	0.03	--
PATIENT_4	<a href="#">chr2:178236873-178587340</a>	18	2	3.57	1.78	0.35	--
PATIENT_4	<a href="#">chr4:62045630-71235540</a>	389	2	3.55	1.78	9.19	<a href="#">EPHA5</a>
PATIENT_4	<a href="#">chr4:81415130-82599606</a>	49	2	3.55	1.78	1.18	<a href="#">PRKG2</a>
PATIENT_4	<a href="#">chr5:110458508-112164920</a>	77	2	3.56	1.78	1.71	APC;CAMK4
PATIENT_4	<a href="#">chr6:97682033-98579156</a>	29	2	3.55	1.78	0.9	--
PATIENT_4	<a href="#">chr7:26371238-26860971</a>	17	2	3.55	1.78	0.49	--
PATIENT_4	<a href="#">chr1:156843678-156936216</a>	54	2	3.54	1.77	0.09	--
PATIENT_4	<a href="#">chr4:96390756-99274560</a>	20	2	3.54	1.77	2.88	--
PATIENT_4	<a href="#">chr4:130025104-134291130</a>	30	2	3.54	1.77	4.27	--
PATIENT_4	<a href="#">chr7:7580282-14679112</a>	186	2	3.53	1.77	7.1	--
PATIENT_4	<a href="#">chr1:213245892-215860334</a>	148	2	3.52	1.76	2.61	--
PATIENT_4	<a href="#">chr2:164299660-169857066</a>	523	2	3.51	1.76	5.56	<a href="#">STK39</a>
PATIENT_4	<a href="#">chr4:100459016-103854704</a>	188	2	3.52	1.76	3.4	<a href="#">NFKB1</a>
PATIENT_4	<a href="#">chr4:114045098-114494458</a>	44	2	3.51	1.76	0.45	--
PATIENT_4	<a href="#">chr7:136351462-137025212</a>	37	2	3.52	1.76	0.67	--
PATIENT_4	<a href="#">chr7:143052751-143085046</a>	5	2	3.51	1.76	0.03	--
PATIENT_4	<a href="#">chr11:18196676-18218072</a>	8	2	3.51	1.76	0.02	--
PATIENT_4	<a href="#">chr11:28308724-30211778</a>	14	2	3.52	1.76	1.9	--
PATIENT_4	<a href="#">chr15:45839337-48186452</a>	292	2	3.52	1.76	2.35	--
PATIENT_4	<a href="#">chr17:71148510-71234912</a>	24	2	3.51	1.76	0.09	--
PATIENT_4	<a href="#">chr2:177993286-178123920</a>	20	2	3.49	1.75	0.13	--
PATIENT_4	<a href="#">chr3:144212356-144322508</a>	30	2	3.5	1.75	0.11	--
PATIENT_4	<a href="#">chr4:72321210-73499454</a>	69	2	3.51	1.75	1.18	--
PATIENT_4	<a href="#">chr4:104051112-104337403</a>	84	2	3.5	1.75	0.29	--
PATIENT_4	<a href="#">chr4:141484272-141704017</a>	31	2	3.5	1.75	0.22	--
PATIENT_4	<a href="#">chr5:57786233-57790618</a>	13	2	3.5	1.75	0	<a href="#">PLK2</a>

PATIENT_4	<a href="#">chr5:65406700-66492088</a>	45	2	3.51	1.75	1.09	--
PATIENT_4	<a href="#">chr5:112878901-115277016</a>	105	2	3.5	1.75	2.4	--
PATIENT_4	<a href="#">chr6:72059751-73959058</a>	71	2	3.49	1.75	1.9	--
PATIENT_4	<a href="#">chr7:7240578-7578789</a>	41	2	3.5	1.75	0.34	--
PATIENT_4	<a href="#">chr8:135881981-139220445</a>	14	2	3.5	1.75	3.34	--
PATIENT_4	<a href="#">chr11:14857235-15217108</a>	26	2	3.5	1.75	0.36	--
PATIENT_4	<a href="#">chr11:22355610-22653050</a>	11	2	3.5	1.75	0.3	<a href="#">FANCF</a>
PATIENT_4	<a href="#">chr11:34427388-34629898</a>	24	2	3.49	1.75	0.2	--
PATIENT_4	<a href="#">chrX:84389267-85189150</a>	46	2	3.49	1.75	0.8	--
PATIENT_4	<a href="#">chr1:170157527-171835916</a>	113	2	3.48	1.74	1.68	--
PATIENT_4	<a href="#">chr6:170686292-170734670</a>	19	2	3.47	1.74	0.05	--
PATIENT_4	<a href="#">chr7:31657342-32057702</a>	24	2	3.48	1.74	0.4	--
PATIENT_4	<a href="#">chr7:77361222-90585362</a>	629	2	3.49	1.74	13.22	--
PATIENT_4	<a href="#">chr8:104122295-116700786</a>	421	2	3.49	1.74	12.58	--
PATIENT_4	<a href="#">chrX:136479734-138729198</a>	79	2	3.49	1.74	2.25	--
PATIENT_4	<a href="#">chrX:146811167-148379798</a>	60	2	3.48	1.74	1.57	--
PATIENT_4	<a href="#">chr1:208192688-208399408</a>	9	2	3.46	1.73	0.21	--
PATIENT_4	<a href="#">chr2:102648108-104809064</a>	24	2	3.46	1.73	2.16	--
PATIENT_4	<a href="#">chr2:133259332-134896893</a>	26	2	3.46	1.73	1.64	--
PATIENT_4	<a href="#">chr2:182469020-187919140</a>	262	2	3.46	1.73	5.45	--
PATIENT_4	<a href="#">chr2:208906359-215711140</a>	392	2	3.45	1.73	6.8	<a href="#">ERBB4</a>
PATIENT_4	<a href="#">chr3:194816200-194892592</a>	28	2	3.47	1.73	0.08	--
PATIENT_4	<a href="#">chr5:38517965-39430130</a>	139	2	3.45	1.73	0.91	<a href="#">LIFR</a>
PATIENT_4	<a href="#">chr6:144654690-147871849</a>	224	2	3.46	1.73	3.22	--
PATIENT_4	<a href="#">chr7:19704483-20632706</a>	44	2	3.46	1.73	0.93	--
PATIENT_4	<a href="#">chr7:38424006-39213572</a>	51	2	3.45	1.73	0.79	--
PATIENT_4	<a href="#">chr7:119972152-126533918</a>	341	2	3.45	1.73	6.56	--
PATIENT_4	<a href="#">chr8:59491996-61354910</a>	72	2	3.46	1.73	1.86	--
PATIENT_4	<a href="#">chr15:58511438-60120830</a>	122	2	3.46	1.73	1.61	--
PATIENT_4	<a href="#">chr21:13909644-16884449</a>	90	2	3.46	1.73	2.97	--
PATIENT_4	<a href="#">chrX:113780207-114329123</a>	47	2	3.46	1.73	0.55	--
PATIENT_4	<a href="#">chr4:42094994-42098153</a>	4	2	3.45	1.72	0	--

PATIENT_4	<a href="#">chr4:155375232-159779892</a>	286	2	3.43	1.72	4.4	--
PATIENT_4	<a href="#">chr6:835839-10155494</a>	25	2	3.44	1.72	1.8	--
PATIENT_4	<a href="#">chr6:47792518-49597368</a>	58	2	3.45	1.72	1.8	--
PATIENT_4	<a href="#">chr7:31345102-31589298</a>	11	2	3.44	1.72	0.24	--
PATIENT_4	<a href="#">chr20:44118962-45067046</a>	132	2	3.43	1.72	0.95	<a href="#">TP53RK</a>
PATIENT_4	<a href="#">chr1:157078734-157302570</a>	36	2	3.41	1.71	0.22	--
PATIENT_4	<a href="#">chr2:75732834-84886352</a>	174	2	3.41	1.71	9.15	--
PATIENT_4	<a href="#">chr3:114017498-114219068</a>	31	2	3.42	1.71	0.2	--
PATIENT_4	<a href="#">chr5:80695402-108719559</a>	881	2	3.41	1.71	28.02	FER;RIOK2
PATIENT_4	<a href="#">chr7:94629166-96162085</a>	110	2	3.42	1.71	1.53	<a href="#">PDK4</a>
PATIENT_4	<a href="#">chr11:11942630-12987766</a>	74	2	3.41	1.71	1.05	--
PATIENT_4	<a href="#">chr11:27479972-27699536</a>	9	2	3.41	1.71	0.22	--
PATIENT_4	<a href="#">chr15:33451613-36605839</a>	80	2	3.42	1.71	3.15	--
PATIENT_4	<a href="#">chr2:152900410-154509336</a>	64	2	3.39	1.7	1.61	--
PATIENT_4	<a href="#">chr3:35698309-35733812</a>	13	2	3.39	1.7	0.04	--
PATIENT_4	<a href="#">chr3:190407958-193560948</a>	105	2	3.39	1.7	3.15	--
PATIENT_4	<a href="#">chr4:114496632-115816800</a>	67	2	3.41	1.7	1.32	<a href="#">CAMK2D</a>
PATIENT_4	<a href="#">chr5:126415434-129549304</a>	189	2	3.39	1.7	3.13	--
PATIENT_4	<a href="#">chr6:46765232-46932561</a>	60	2	3.4	1.7	0.17	--
PATIENT_4	<a href="#">chr7:145444938-146967190</a>	15	2	3.4	1.7	1.52	--
PATIENT_4	<a href="#">chr8:61659870-61695836</a>	4	2	3.4	1.7	0.04	--
PATIENT_4	<a href="#">chr8:119461001-120324882</a>	21	2	3.4	1.7	0.86	--
PATIENT_4	<a href="#">chr9:109862402-109961715</a>	21	2	3.4	1.7	0.1	--
PATIENT_4	<a href="#">chr17:61922822-62307196</a>	49	2	3.4	1.7	0.38	<a href="#">PRKCA</a>
PATIENT_4	<a href="#">chr18:8234110-8773688</a>	30	2	3.39	1.7	0.54	--
PATIENT_4	<a href="#">chr3:110678267-113085915</a>	38	2	3.38	1.69	2.41	--
PATIENT_4	<a href="#">chr4:120277160-123065710</a>	171	2	3.38	1.69	2.79	--
PATIENT_4	<a href="#">chr4:123311285-126593152</a>	247	2	3.38	1.69	3.28	<a href="#">IL2</a>
PATIENT_4	<a href="#">chr5:63532456-64886434</a>	73	2	3.39	1.69	1.35	--
PATIENT_4	<a href="#">chr5:145814946-147996752</a>	187	2	3.38	1.69	2.18	<a href="#">SPINK1</a>
PATIENT_4	<a href="#">chr7:33158923-35910394</a>	109	2	3.38	1.69	2.75	--
PATIENT_4	<a href="#">chr7:37955044-38323591</a>	26	2	3.37	1.69	0.37	--
PATIENT_4	<a href="#">chr8:49665724-52483230</a>	45	2	3.37	1.69	2.82	--

PATIENT_4	<a href="#">chr14:46190186-46459050</a>	10	2	3.38	1.69	0.27	--
PATIENT_4	<a href="#">chrX:35847946-38029846</a>	129	2	3.38	1.69	2.18	--
PATIENT_4	<a href="#">chrX:80256822-80439392</a>	13	2	3.39	1.69	0.18	--
PATIENT_4	<a href="#">chr4:134293167-139382588</a>	43	2	3.37	1.68	5.09	--
PATIENT_4	<a href="#">chr5:57826130-61035518</a>	93	2	3.36	1.68	3.21	--
PATIENT_4	<a href="#">chr6:49681484-52121658</a>	156	2	3.35	1.68	2.44	--
PATIENT_4	<a href="#">chr6:155648042-155818581</a>	18	2	3.35	1.68	0.17	--
PATIENT_4	<a href="#">chr11:35641643-44222319</a>	191	2	3.35	1.68	8.58	<a href="#">EXT2</a>
PATIENT_4	<a href="#">chrX:96054012-96740937</a>	23	2	3.37	1.68	0.69	--
PATIENT_4	<a href="#">chrX:122146122-122485978</a>	52	2	3.36	1.68	0.34	--
PATIENT_4	<a href="#">chrX:123414947-123925172</a>	24	2	3.35	1.68	0.51	--
PATIENT_4	<a href="#">chr1:241500947-242281362</a>	30	2	3.33	1.67	0.78	<a href="#">AKT3</a>
PATIENT_4	<a href="#">chr2:101781574-102515400</a>	115	2	3.34	1.67	0.73	--
PATIENT_4	<a href="#">chr2:191042776-196880144</a>	257	2	3.33	1.67	5.84	<a href="#">STK17B</a>
PATIENT_4	<a href="#">chr2:204444394-206270583</a>	39	2	3.34	1.67	1.83	--
PATIENT_4	<a href="#">chr3:127339880-127350786</a>	10	2	3.34	1.67	0.01	--
PATIENT_4	<a href="#">chr3:127363714-127403552</a>	10	2	3.34	1.67	0.04	--
PATIENT_4	<a href="#">chr3:131298690-133921294</a>	349	2	3.33	1.67	2.62	NEK11;PIK3R4
PATIENT_4	<a href="#">chr4:95366370-96294766</a>	56	2	3.33	1.67	0.93	<a href="#">BMPR1B</a>
PATIENT_4	<a href="#">chr4:171218670-176134092</a>	96	2	3.34	1.67	4.92	--
PATIENT_4	<a href="#">chr4:176135395-183911676</a>	118	2	3.34	1.67	7.78	--
PATIENT_4	<a href="#">chr5:56188252-56212766</a>	13	2	3.35	1.67	0.02	<a href="#">MAP3K1</a>
PATIENT_4	<a href="#">chr5:158058711-158686314</a>	47	2	3.35	1.67	0.63	<a href="#">EBF1</a>
PATIENT_4	<a href="#">chr6:44905540-46763912</a>	74	2	3.35	1.67	1.86	--
PATIENT_4	<a href="#">chr8:75435024-79740944</a>	96	2	3.34	1.67	4.31	--
PATIENT_4	<a href="#">chr15:69982385-70018274</a>	7	2	3.33	1.67	0.04	--
PATIENT_4	<a href="#">chr17:52689464-53064164</a>	10	2	3.34	1.67	0.37	<a href="#">MSI2</a>
PATIENT_4	<a href="#">chr20:55383159-57781808</a>	209	2	3.33	1.67	2.4	<a href="#">GNAS</a>
PATIENT_4	<a href="#">chrX:104365268-106003805</a>	111	2	3.34	1.67	1.64	--
PATIENT_4	<a href="#">chrX:131016442-131670173</a>	42	2	3.34	1.67	0.65	--
PATIENT_4	<a href="#">chr2:107821807-108276636</a>	29	2	3.32	1.66	0.45	--
PATIENT_4	<a href="#">chr3:194456190-194703043</a>	64	2	3.32	1.66	0.25	--

PATIENT_4	<a href="#">chr4:116216784-119476176</a>	40	2	3.32	1.66	3.26	--
PATIENT_4	<a href="#">chr5:7679363-9683068</a>	81	2	3.33	1.66	2	--
PATIENT_4	<a href="#">chr5:42795013-42879863</a>	18	2	3.32	1.66	0.08	--
PATIENT_4	<a href="#">chr5:148391376-148411940</a>	8	2	3.31	1.66	0.02	--
PATIENT_4	<a href="#">chr5:155689148-156118911</a>	8	2	3.31	1.66	0.43	--
PATIENT_4	<a href="#">chr7:37913696-37920532</a>	5	2	3.32	1.66	0.01	--
PATIENT_4	<a href="#">chr8:117726476-118621334</a>	41	2	3.33	1.66	0.89	--
PATIENT_4	<a href="#">chr9:72425988-73490518</a>	20	2	3.32	1.66	1.06	--
PATIENT_4	<a href="#">chr16:13921642-13939162</a>	12	2	3.32	1.66	0.02	<a href="#">ERCC4</a>
PATIENT_4	<a href="#">chrX:79823566-79950726</a>	39	2	3.32	1.66	0.13	--
PATIENT_4	<a href="#">chrX:109811439-110887574</a>	92	2	3.32	1.66	1.08	<a href="#">PAK3</a>
PATIENT_4	<a href="#">chrX:150322806-150590240</a>	13	2	3.32	1.66	0.27	--
PATIENT_4	<a href="#">chr2:130560006-130589300</a>	5	2	3.3	1.65	0.03	--
PATIENT_4	<a href="#">chr3:113120670-113839996</a>	132	2	3.3	1.65	0.72	--
PATIENT_4	<a href="#">chr3:155323462-156380907</a>	76	2	3.29	1.65	1.06	--
PATIENT_4	<a href="#">chr3:188441991-188447838</a>	3	2	3.3	1.65	0.01	--
PATIENT_4	<a href="#">chr4:111617576-111702074</a>	20	2	3.31	1.65	0.08	--
PATIENT_4	<a href="#">chr4:144328498-144693752</a>	54	2	3.3	1.65	0.37	--
PATIENT_4	<a href="#">chr6:74489710-79827174</a>	264	2	3.31	1.65	5.34	--
PATIENT_4	<a href="#">chr8:131197104-133927281</a>	175	2	3.3	1.65	2.73	--
PATIENT_4	<a href="#">chr11:2927062-2979820</a>	16	2	3.29	1.65	0.05	<a href="#">CARS</a>
PATIENT_4	<a href="#">chr11:26699650-27033661</a>	4	2	3.29	1.65	0.33	--
PATIENT_4	<a href="#">chr15:68973004-69128911</a>	15	2	3.29	1.65	0.16	--
PATIENT_4	<a href="#">chrX:107153647-107864224</a>	141	2	3.3	1.65	0.71	--
PATIENT_4	<a href="#">chr1:145875402-145882772</a>	4	2	3.29	1.64	0.01	--
PATIENT_4	<a href="#">chr2:207018352-207697258</a>	86	2	3.29	1.64	0.68	--
PATIENT_4	<a href="#">chr5:17328930-31520770</a>	109	2	3.27	1.64	14.19	--
PATIENT_4	<a href="#">chr5:124001477-124007200</a>	4	2	3.27	1.64	0.01	--
PATIENT_4	<a href="#">chr6:137367494-137569820</a>	19	2	3.29	1.64	0.2	--
PATIENT_4	<a href="#">chr7:111168440-117218424</a>	292	2	3.28	1.64	6.05	<a href="#">MET</a>
PATIENT_4	<a href="#">chr7:143781626-144010974</a>	6	2	3.28	1.64	0.23	--
PATIENT_4	<a href="#">chr8:79879704-80739609</a>	6	2	3.28	1.64	0.86	--
PATIENT_4	<a href="#">chr8:82358156-93998355</a>	389	2	3.28	1.64	11.64	<a href="#">PSKH2;RIPK2</a>

PATIENT_4	<a href="#">chr8:121229297-121604732</a>	77	2	3.29	1.64	0.38	--
PATIENT_4	<a href="#">chr9:14609624-14664254</a>	6	2	3.28	1.64	0.05	--
PATIENT_4	<a href="#">chr15:54177710-55331918</a>	71	2	3.29	1.64	1.15	<a href="#">TCF12</a>
PATIENT_4	<a href="#">chr17:52276467-52295062</a>	10	2	3.27	1.64	0.02	--
PATIENT_4	<a href="#">chr17:58375322-58849430</a>	27	2	3.28	1.64	0.47	--
PATIENT_4	<a href="#">chr1:166776881-169435177</a>	294	2	3.26	1.63	2.66	<a href="#">SCYL3</a>
PATIENT_4	<a href="#">chr3:102127922-102660520</a>	53	2	3.26	1.63	0.53	--
PATIENT_4	<a href="#">chr4:44326253-46085444</a>	45	2	3.26	1.63	1.76	--
PATIENT_4	<a href="#">chr6:46936480-47082938</a>	19	2	3.27	1.63	0.15	--
PATIENT_4	<a href="#">chr9:97660367-97815210</a>	31	2	3.27	1.63	0.15	--
PATIENT_4	<a href="#">chr12:70953424-71343159</a>	19	2	3.27	1.63	0.39	--
PATIENT_4	<a href="#">chr2:159800848-162404619</a>	212	2	3.23	1.62	2.6	--
PATIENT_4	<a href="#">chr3:114488286-114708074</a>	57	2	3.25	1.62	0.22	--
PATIENT_4	<a href="#">chr3:173955071-180430834</a>	115	2	3.25	1.62	6.48	<a href="#">PIK3CA</a>
PATIENT_4	<a href="#">chr5:11450178-14459032</a>	120	2	3.24	1.62	3.01	<a href="#">TRIO</a>
PATIENT_4	<a href="#">chr5:118553402-122939508</a>	161	2	3.25	1.62	4.39	<a href="#">CSNK1G3</a>
PATIENT_4	<a href="#">chr6:39421480-39796512</a>	21	2	3.24	1.62	0.38	--
PATIENT_4	<a href="#">chr6:128430449-134415255</a>	412	2	3.24	1.62	5.98	--
PATIENT_4	<a href="#">chr11:9554696-11820310</a>	189	2	3.25	1.62	2.27	<a href="#">WEE1</a>
PATIENT_4	<a href="#">chr11:14257495-14497123</a>	35	2	3.24	1.62	0.24	--
PATIENT_4	<a href="#">chrX:32569543-34871095</a>	30	2	3.23	1.62	2.3	--
PATIENT_4	<a href="#">chr2:155263550-159630706</a>	141	2	3.23	1.61	4.37	ACVR1;ACVR1C
PATIENT_4	<a href="#">chr3:148611494-150285270</a>	64	2	3.22	1.61	1.67	--
PATIENT_4	<a href="#">chr3:157622116-162704400</a>	284	2	3.21	1.61	5.08	<a href="#">MLF1</a>
PATIENT_4	<a href="#">chr3:171799431-173537856</a>	101	2	3.21	1.61	1.74	--
PATIENT_4	<a href="#">chr3:180984568-182188676</a>	80	2	3.22	1.61	1.2	--
PATIENT_4	<a href="#">chr4:78195440-80548220</a>	169	2	3.21	1.61	2.35	<a href="#">BMP2K</a>
PATIENT_4	<a href="#">chr4:164467010-164612508</a>	9	2	3.23	1.61	0.15	--
PATIENT_4	<a href="#">chr6:15701244-15760325</a>	6	2	3.22	1.61	0.06	--
PATIENT_4	<a href="#">chr7:47912024-49785707</a>	141	2	3.21	1.61	1.87	--
PATIENT_4	<a href="#">chr11:3336946-3349434</a>	14	2	3.22	1.61	0.01	--
PATIENT_4	<a href="#">chr17:56179372-56516658</a>	19	2	3.23	1.61	0.34	--

PATIENT_4	<a href="#">chr17:71440700-71493909</a>	37	2	3.23	1.61	0.05	--
PATIENT_4	<a href="#">chrX:38032148-38431817</a>	31	2	3.22	1.61	0.4	--
PATIENT_4	<a href="#">chr1:70064046-70259327</a>	12	2	3.2	1.6	0.2	--
PATIENT_4	<a href="#">chr2:68815855-69274007</a>	51	2	3.2	1.6	0.46	--
PATIENT_4	<a href="#">chr3:135359736-135424008</a>	14	2	3.19	1.6	0.06	--
PATIENT_4	<a href="#">chr6:25393078-26091584</a>	101	2	3.21	1.6	0.7	--
PATIENT_4	<a href="#">chr6:38753084-39088353</a>	98	2	3.19	1.6	0.34	--
PATIENT_4	<a href="#">chr6:41143096-41173089</a>	14	2	3.21	1.6	0.03	--
PATIENT_4	<a href="#">chr6:83659460-86324444</a>	222	2	3.21	1.6	2.66	--
PATIENT_4	<a href="#">chr6:152696906-154373366</a>	115	2	3.19	1.6	1.68	--
PATIENT_4	<a href="#">chr6:168008173-168094816</a>	30	2	3.19	1.6	0.09	<a href="#">MLLT4</a>
PATIENT_4	<a href="#">chr8:62789439-64148128</a>	20	2	3.21	1.6	1.36	--
PATIENT_4	<a href="#">chr11:31768900-32395740</a>	24	2	3.2	1.6	0.63	<a href="#">WT1</a>
PATIENT_4	<a href="#">chr11:72800143-72857135</a>	4	2	3.2	1.6	0.06	--
PATIENT_4	<a href="#">chr15:24804948-25844930</a>	16	2	3.19	1.6	1.04	--
PATIENT_4	<a href="#">chr16:37480-51205</a>	17	2	3.2	1.6	0.01	--
PATIENT_4	<a href="#">chr17:61252720-61522872</a>	16	2	3.21	1.6	0.27	--
PATIENT_4	<a href="#">chrX:72713992-72928402</a>	6	2	3.2	1.6	0.21	--
PATIENT_4	<a href="#">chr2:62581936-63133662</a>	34	2	3.17	1.59	0.55	--
PATIENT_4	<a href="#">chr2:114387248-118582338</a>	81	2	3.18	1.59	4.2	--
PATIENT_4	<a href="#">chr2:175330596-176618782</a>	60	2	3.19	1.59	1.29	--
PATIENT_4	<a href="#">chr2:198301524-201243615</a>	143	2	3.17	1.59	2.94	--
PATIENT_4	<a href="#">chr3:186025194-186194496</a>	42	2	3.19	1.59	0.17	--
PATIENT_4	<a href="#">chr4:55256594-55682062</a>	52	2	3.18	1.59	0.43	KDR;KIT
PATIENT_4	<a href="#">chr4:81212652-81341557</a>	3	2	3.19	1.59	0.13	--
PATIENT_4	<a href="#">chr6:111727962-121697190</a>	524	2	3.18	1.59	9.97	FRK;FYN;GOPC;ROS1
PATIENT_4	<a href="#">chr10:112757332-112761476</a>	4	2	3.18	1.59	0	--
PATIENT_4	<a href="#">chr11:72372838-72528762</a>	7	2	3.18	1.59	0.16	--
PATIENT_4	<a href="#">chr17:42760711-42872928</a>	24	2	3.19	1.59	0.11	--
PATIENT_4	<a href="#">chr17:50700186-51183516</a>	13	2	3.18	1.59	0.48	<a href="#">HLF</a>
PATIENT_4	<a href="#">chr20:49441364-49573084</a>	12	2	3.19	1.59	0.13	--
PATIENT_4	<a href="#">chrX:129587057-130248269</a>	47	2	3.18	1.59	0.66	--

PATIENT_4	<a href="#">chrX:149428902-149674892</a>	28	2	3.19	1.59	0.25	--
PATIENT_4	<a href="#">chr1:159988122-160195060</a>	23	2	3.15	1.58	0.21	--
PATIENT_4	<a href="#">chr2:63202640-64064578</a>	65	2	3.16	1.58	0.86	--
PATIENT_4	<a href="#">chr2:95509896-95952130</a>	10	2	3.17	1.58	0.44	--
PATIENT_4	<a href="#">chr2:189683304-190942149</a>	123	2	3.17	1.58	1.26	<a href="#">PMS1</a>
PATIENT_4	<a href="#">chr5:72779837-73966403</a>	68	2	3.17	1.58	1.19	--
PATIENT_4	<a href="#">chr5:76970108-77820710</a>	43	2	3.16	1.58	0.85	--
PATIENT_4	<a href="#">chr5:132764439-133320509</a>	5	2	3.16	1.58	0.56	--
PATIENT_4	<a href="#">chr8:61856151-62631079</a>	59	2	3.17	1.58	0.77	--
PATIENT_4	<a href="#">chr13:35022666-35100294</a>	8	2	3.17	1.58	0.08	--
PATIENT_4	<a href="#">chr16:14553410-14607856</a>	12	2	3.15	1.58	0.05	--
PATIENT_4	<a href="#">chr22:21670900-21679316</a>	5	2	3.17	1.58	0.01	--
PATIENT_4	<a href="#">chrX:31049905-31435394</a>	26	2	3.15	1.58	0.39	--
PATIENT_4	<a href="#">chrX:57330056-57532006</a>	11	2	3.17	1.58	0.2	--
PATIENT_4	<a href="#">chr1:225259378-225909307</a>	44	2	3.14	1.57	0.65	<a href="#">CDC42BPA</a>
PATIENT_4	<a href="#">chr2:54930754-54991626</a>	16	2	3.13	1.57	0.06	--
PATIENT_4	<a href="#">chr3:142713730-142813840</a>	24	2	3.15	1.57	0.1	--
PATIENT_4	<a href="#">chr4:43362-129702</a>	20	2	3.14	1.57	0.09	--
PATIENT_4	<a href="#">chr6:110531291-110870210</a>	37	2	3.15	1.57	0.34	--
PATIENT_4	<a href="#">chr11:68061810-68125935</a>	19	2	3.14	1.57	0.06	--
PATIENT_4	<a href="#">chr14:87476041-87504498</a>	9	2	3.15	1.57	0.03	--
PATIENT_4	<a href="#">chr16:5083524-7700646</a>	19	2	3.13	1.57	2.62	--
PATIENT_4	<a href="#">chr17:55478246-55510930</a>	20	2	3.14	1.57	0.03	--
PATIENT_4	<a href="#">chrX:134119852-134543170</a>	40	2	3.14	1.57	0.42	--
PATIENT_4	<a href="#">chr1:223207054-223821647</a>	115	2	3.13	1.56	0.61	--
PATIENT_4	<a href="#">chr2:47167686-47257064</a>	13	2	3.11	1.56	0.09	--
PATIENT_4	<a href="#">chr2:66516492-68658541</a>	79	2	3.11	1.56	2.14	--
PATIENT_4	<a href="#">chr3:95205324-98189474</a>	32	2	3.11	1.56	2.98	--
PATIENT_4	<a href="#">chr4:129319086-129413034</a>	10	2	3.13	1.56	0.09	--
PATIENT_4	<a href="#">chr5:5193823-6431528</a>	73	2	3.11	1.56	1.24	--
PATIENT_4	<a href="#">chr5:142130575-145182836</a>	58	2	3.12	1.56	3.05	--
PATIENT_4	<a href="#">chr6:20757526-21339144</a>	12	2	3.12	1.56	0.58	--
PATIENT_4	<a href="#">chr9:84787454-85177638</a>	32	2	3.12	1.56	0.39	--

PATIENT_4	<a href="#">chr9:86507132-87517247</a>	46	2	3.13	1.56	1.01	<a href="#">NTRK2</a>
PATIENT_4	<a href="#">chr11:20472317-20656122</a>	22	2	3.12	1.56	0.18	--
PATIENT_4	<a href="#">chr20:50214642-51621742</a>	21	2	3.13	1.56	1.41	--
PATIENT_4	<a href="#">chr1:215888898-217413897</a>	24	2	3.09	1.55	1.52	--
PATIENT_4	<a href="#">chr2:124499722-127167944</a>	28	2	3.09	1.55	2.67	--
PATIENT_4	<a href="#">chr4:119828554-120167276</a>	36	2	3.1	1.55	0.34	--
PATIENT_4	<a href="#">chr5:33973936-37094908</a>	308	2	3.1	1.55	3.12	--
PATIENT_4	<a href="#">chr8:180898-391364</a>	17	2	3.1	1.55	0.21	--
PATIENT_4	<a href="#">chr8:52486424-53760536</a>	80	2	3.1	1.55	1.27	--
PATIENT_4	<a href="#">chr8:97242078-98359040</a>	42	2	3.1	1.55	1.12	--
PATIENT_4	<a href="#">chr9:71523378-72152708</a>	50	2	3.11	1.55	0.63	--
PATIENT_4	<a href="#">chr11:45912196-46062312</a>	18	2	3.1	1.55	0.15	--
PATIENT_4	<a href="#">chr15:94681733-96755564</a>	21	2	3.1	1.55	2.07	--
PATIENT_4	<a href="#">chr16:9764540-9939688</a>	24	2	3.09	1.55	0.18	--
PATIENT_4	<a href="#">chrX:106084884-106373116</a>	35	2	3.1	1.55	0.29	--
PATIENT_4	<a href="#">chrX:115217573-115481922</a>	5	2	3.1	1.55	0.26	--
PATIENT_4	<a href="#">chr1:20286906-20287684</a>	3	2	3.07	1.54	0	--
PATIENT_4	<a href="#">chr1:179746282-179968294</a>	19	2	3.08	1.54	0.22	--
PATIENT_4	<a href="#">chr2:72260014-72822016</a>	21	2	3.08	1.54	0.56	--
PATIENT_4	<a href="#">chr3:123942582-124080838</a>	16	2	3.08	1.54	0.14	--
PATIENT_4	<a href="#">chr6:56565028-64632110</a>	243	2	3.08	1.54	8.07	--
PATIENT_4	<a href="#">chr8:126084740-126263597</a>	41	2	3.07	1.54	0.18	--
PATIENT_4	<a href="#">chr13:46243586-46263510</a>	8	2	3.07	1.54	0.02	--
PATIENT_4	<a href="#">chr17:62444800-62482708</a>	8	2	3.08	1.54	0.04	--
PATIENT_4	<a href="#">chr17:62772366-63944162</a>	136	2	3.08	1.54	1.17	--
PATIENT_4	<a href="#">chr20:29808980-29852470</a>	17	2	3.07	1.54	0.04	--
PATIENT_4	<a href="#">chr2:97776344-98294820</a>	56	2	3.06	1.53	0.52	--
PATIENT_4	<a href="#">chr2:225047274-225087650</a>	13	2	3.05	1.53	0.04	--
PATIENT_4	<a href="#">chr3:87372580-87408248</a>	11	2	3.05	1.53	0.04	--
PATIENT_4	<a href="#">chr4:126628193-128973428</a>	60	2	3.07	1.53	2.35	--
PATIENT_4	<a href="#">chr5:53874856-54504546</a>	32	2	3.06	1.53	0.63	--
PATIENT_4	<a href="#">chr6:350070-582738</a>	29	2	3.07	1.53	0.23	<a href="#">IRF4</a>
PATIENT_4	<a href="#">chr6:47087786-47104707</a>	9	2	3.06	1.53	0.02	--

PATIENT_4	<a href="#">chr7:30503292-30639932</a>	21	2	3.06	1.53	0.14	--
PATIENT_4	<a href="#">chr9:125385314-125681084</a>	11	2	3.05	1.53	0.3	--
PATIENT_4	<a href="#">chr11:19911382-20366218</a>	62	2	3.06	1.53	0.45	--
PATIENT_4	<a href="#">chr12:73956273-74186396</a>	42	2	3.05	1.53	0.23	--
PATIENT_4	<a href="#">chr13:114020263-114109832</a>	43	2	3.05	1.53	0.09	--
PATIENT_4	<a href="#">chr17:53640911-53651023</a>	11	2	3.07	1.53	0.01	--
PATIENT_4	<a href="#">chrX:83610226-84249010</a>	20	2	3.06	1.53	0.64	--
PATIENT_4	<a href="#">chr1:102042948-103964678</a>	94	2	3.04	1.52	1.92	--
PATIENT_4	<a href="#">chr1:224486884-224555485</a>	14	2	3.03	1.52	0.07	--
PATIENT_4	<a href="#">chr2:104840244-105082596</a>	15	2	3.05	1.52	0.24	--
PATIENT_4	<a href="#">chr3:99151456-101952076</a>	235	2	3.04	1.52	2.8	<a href="#">TFG</a>
PATIENT_4	<a href="#">chr6:135828640-136623934</a>	29	2	3.04	1.52	0.8	--
PATIENT_4	<a href="#">chr8:146127060-146250272</a>	16	2	3.05	1.52	0.12	--
PATIENT_4	<a href="#">chr9:90846834-91152886</a>	25	2	3.05	1.52	0.31	--
PATIENT_4	<a href="#">chr14:106184774-106354289</a>	23	2	3.04	1.52	0.17	--
PATIENT_4	<a href="#">chr15:23135440-23475688</a>	18	2	3.03	1.52	0.34	--
PATIENT_4	<a href="#">chr15:49290405-49804500</a>	98	2	3.05	1.52	0.51	--
PATIENT_4	<a href="#">chr15:55608216-56797124</a>	73	2	3.03	1.52	1.19	--
PATIENT_4	<a href="#">chr16:11045402-11062313</a>	4	2	3.04	1.52	0.02	--
PATIENT_4	<a href="#">chr17:68704380-70427333</a>	274	2	3.04	1.52	1.72	--
PATIENT_4	<a href="#">chr18:20896657-21029156</a>	8	2	3.04	1.52	0.13	<a href="#">ZNF521</a>
PATIENT_4	<a href="#">chrX:21665657-21781469</a>	9	2	3.05	1.52	0.12	--
PATIENT_4	<a href="#">chr1:179974154-180034588</a>	26	2	3.03	1.51	0.06	--
PATIENT_4	<a href="#">chr1:235033450-236118352</a>	165	2	3.01	1.51	1.08	--
PATIENT_4	<a href="#">chr2:98564554-98779066</a>	29	2	3.02	1.51	0.21	--
PATIENT_4	<a href="#">chr2:196892826-197966058</a>	112	2	3.02	1.51	1.07	--
PATIENT_4	<a href="#">chr5:32774798-33611946</a>	32	2	3.02	1.51	0.84	--
PATIENT_4	<a href="#">chr5:76366044-76823770</a>	48	2	3.02	1.51	0.46	--
PATIENT_4	<a href="#">chr6:109894452-110253064</a>	86	2	3.01	1.51	0.36	--
PATIENT_4	<a href="#">chr8:99274461-99335440</a>	12	2	3.02	1.51	0.06	--
PATIENT_4	<a href="#">chr9:79004724-81529812</a>	141	2	3.02	1.51	2.53	<a href="#">GNAQ</a>
PATIENT_4	<a href="#">chr9:124867504-124986213</a>	32	2	3.01	1.51	0.12	--

PATIENT_4	<a href="#">chr12:81948739-87463712</a>	194	2	3.02	1.51	5.51	--
PATIENT_4	<a href="#">chrX:71466636-72350600</a>	52	2	3.01	1.51	0.88	--
PATIENT_4	<a href="#">chr2:119776538-119813938</a>	5	2	3.01	1.5	0.04	--
PATIENT_4	<a href="#">chr2:240895002-240905952</a>	9	2	2.99	1.5	0.01	--
PATIENT_4	<a href="#">chr3:74434579-74652926</a>	13	2	3	1.5	0.22	--
PATIENT_4	<a href="#">chr4:74921378-75242781</a>	34	2	3	1.5	0.32	--
PATIENT_4	<a href="#">chr4:108860754-109051050</a>	7	2	3	1.5	0.19	--
PATIENT_4	<a href="#">chr4:154690724-154926515</a>	54	2	3	1.5	0.24	--
PATIENT_4	<a href="#">chr4:170870889-170911474</a>	10	2	3	1.5	0.04	--
PATIENT_4	<a href="#">chr6:100475666-101004228</a>	17	2	3	1.5	0.53	--
PATIENT_4	<a href="#">chr7:106300249-110948652</a>	298	2	3	1.5	4.65	--
PATIENT_4	<a href="#">chr7:155297419-156322296</a>	27	2	3.01	1.5	1.02	--
PATIENT_4	<a href="#">chr8:66814313-67251806</a>	24	2	3.01	1.5	0.44	--
PATIENT_4	<a href="#">chr9:99243854-99495840</a>	64	2	2.99	1.5	0.25	<a href="#">XPA</a>
PATIENT_4	<a href="#">chr11:48284886-48467842</a>	19	2	3	1.5	0.18	--
PATIENT_4	<a href="#">chr15:31146145-31750003</a>	51	2	3.01	1.5	0.6	--
PATIENT_4	<a href="#">chr17:42553332-42613958</a>	18	2	3	1.5	0.06	--
PATIENT_4	<a href="#">chr17:59506278-59584119</a>	7	2	3	1.5	0.08	--
PATIENT_4	<a href="#">chr18:8774722-8811476</a>	8	2	3.01	1.5	0.04	--
PATIENT_4	<a href="#">chr1:77288578-77448728</a>	13	2	2.99	1.49	0.16	--
PATIENT_4	<a href="#">chr1:160823975-161305667</a>	38	2	2.99	1.49	0.48	<a href="#">DDR2</a>
PATIENT_4	<a href="#">chr2:55910001-56453057</a>	27	2	2.98	1.49	0.54	--
PATIENT_4	<a href="#">chr2:97147590-97630944</a>	81	2	2.98	1.49	0.48	--
PATIENT_4	<a href="#">chr2:225351156-226086554</a>	54	2	2.97	1.49	0.74	--
PATIENT_4	<a href="#">chr4:166350757-166628112</a>	27	2	2.99	1.49	0.28	--
PATIENT_4	<a href="#">chr4:170275399-170854984</a>	52	2	2.98	1.49	0.58	--
PATIENT_4	<a href="#">chr6:127649612-127836172</a>	22	2	2.99	1.49	0.19	--
PATIENT_4	<a href="#">chr8:99537324-101658454</a>	195	2	2.99	1.49	2.12	<a href="#">COX6C</a>
PATIENT_4	<a href="#">chr14:35838070-35855700</a>	9	2	2.98	1.49	0.02	--
PATIENT_4	<a href="#">chr22:26580902-26640286</a>	10	2	2.99	1.49	0.06	--
PATIENT_4	<a href="#">chrX:16975438-18123396</a>	57	2	2.97	1.49	1.15	--
PATIENT_4	<a href="#">chrX:108505814-109471128</a>	77	2	2.97	1.49	0.97	<a href="#">GUCY2F</a>

PATIENT_4	<a href="#">chrX:135261308-135657372</a>	78	2	2.97	1.49	0.4	--
PATIENT_4	<a href="#">chr1:78731680-84555098</a>	101	2	2.96	1.48	5.82	<a href="#">PRKACB</a>
PATIENT_4	<a href="#">chr1:247073152-247119324</a>	24	2	2.96	1.48	0.05	--
PATIENT_4	<a href="#">chr3:150340640-153659766</a>	310	2	2.96	1.48	3.32	--
PATIENT_4	<a href="#">chr3:184020800-184161761</a>	33	2	2.96	1.48	0.14	--
PATIENT_4	<a href="#">chr4:152706906-152860072</a>	29	2	2.96	1.48	0.15	--
PATIENT_4	<a href="#">chr4:153552134-154113046</a>	41	2	2.96	1.48	0.56	<a href="#">FBXW7</a>
PATIENT_4	<a href="#">chr5:33631843-33927658</a>	17	2	2.96	1.48	0.3	--
PATIENT_4	<a href="#">chr5:43526527-49772680</a>	81	2	2.96	1.48	6.25	--
PATIENT_4	<a href="#">chr7:136238508-136351263</a>	7	2	2.96	1.48	0.11	--
PATIENT_4	<a href="#">chr9:92646341-93158202</a>	23	2	2.95	1.48	0.51	<a href="#">SYK</a>
PATIENT_4	<a href="#">chr9:118531150-122370448</a>	89	2	2.95	1.48	3.84	--
PATIENT_4	<a href="#">chr11:88600712-89088748</a>	41	2	2.96	1.48	0.49	--
PATIENT_4	<a href="#">chr17:42125534-42188357</a>	10	2	2.96	1.48	0.06	--
PATIENT_4	<a href="#">chr17:57022680-57327514</a>	45	2	2.97	1.48	0.3	<a href="#">BRIP1</a>
PATIENT_4	<a href="#">chr17:75725830-75735328</a>	11	2	2.96	1.48	0.01	--
PATIENT_4	<a href="#">chr18:28772007-29577694</a>	53	2	2.95	1.48	0.81	--
PATIENT_4	<a href="#">chr20:33365941-33445342</a>	7	2	2.95	1.48	0.08	--
PATIENT_4	<a href="#">chr20:42546484-43177094</a>	102	2	2.95	1.48	0.63	ADA;STK4
PATIENT_4	<a href="#">chr20:43350674-43871188</a>	111	2	2.96	1.48	0.52	--
PATIENT_4	<a href="#">chrX:10161574-16080291</a>	377	2	2.97	1.48	5.92	<a href="#">BMX</a>
PATIENT_4	<a href="#">chr1:228570414-228895714</a>	21	2	2.93	1.47	0.33	--
PATIENT_4	<a href="#">chr2:99632530-100292037</a>	23	2	2.95	1.47	0.66	--
PATIENT_4	<a href="#">chr3:124935657-125697888</a>	89	2	2.95	1.47	0.76	KALRN;MYLK
PATIENT_4	<a href="#">chr4:35751772-37116960</a>	52	2	2.94	1.47	1.37	--
PATIENT_4	<a href="#">chr4:53940009-54610179</a>	39	2	2.95	1.47	0.67	CHIC2;FIP1L1
PATIENT_4	<a href="#">chr4:56003450-56871618</a>	80	2	2.94	1.47	0.87	--
PATIENT_4	<a href="#">chr5:110124809-110456020</a>	8	2	2.94	1.47	0.33	--
PATIENT_4	<a href="#">chr5:151035896-153706922</a>	72	2	2.94	1.47	2.67	<a href="#">SPARC</a>
PATIENT_4	<a href="#">chr6:135312810-135757654</a>	52	2	2.95	1.47	0.44	<a href="#">MYB</a>
PATIENT_4	<a href="#">chr7:16427332-16760144</a>	28	2	2.94	1.47	0.33	--
PATIENT_4	<a href="#">chr7:45896744-47308339</a>	16	2	2.93	1.47	1.41	--

PATIENT_4	<a href="#">chr9:106925-168880</a>	11	2	2.94	1.47	0.06	--
PATIENT_4	<a href="#">chr11:7774284-8241469</a>	60	2	2.94	1.47	0.47	--
PATIENT_4	<a href="#">chr15:66165993-66273456</a>	14	2	2.93	1.47	0.11	--
PATIENT_4	<a href="#">chrX:125781495-128703792</a>	62	2	2.93	1.47	2.92	--
PATIENT_4	<a href="#">chr1:71303362-74782217</a>	75	2	2.92	1.46	3.48	<a href="#">TNNI3K</a>
PATIENT_4	<a href="#">chr1:205329528-206450354</a>	159	2	2.93	1.46	1.12	--
PATIENT_4	<a href="#">chr1:221223051-221234904</a>	5	2	2.91	1.46	0.01	--
PATIENT_4	<a href="#">chr1:229109326-229198215</a>	26	2	2.91	1.46	0.09	--
PATIENT_4	<a href="#">chr2:228458328-228589407</a>	19	2	2.92	1.46	0.13	--
PATIENT_4	<a href="#">chr3:140545632-142143598</a>	73	2	2.92	1.46	1.6	--
PATIENT_4	<a href="#">chr5:37552414-38517750</a>	39	2	2.93	1.46	0.97	<a href="#">LIFR</a>
PATIENT_4	<a href="#">chr6:52988905-53070528</a>	19	2	2.93	1.46	0.08	<a href="#">ICK</a>
PATIENT_4	<a href="#">chr6:70127706-70128091</a>	4	2	2.91	1.46	0	--
PATIENT_4	<a href="#">chr6:71047264-71722785</a>	65	2	2.91	1.46	0.68	--
PATIENT_4	<a href="#">chr7:36413964-37747388</a>	70	2	2.93	1.46	1.33	--
PATIENT_4	<a href="#">chr7:97201514-97326547</a>	14	2	2.92	1.46	0.13	--
PATIENT_4	<a href="#">chr8:141818334-141970050</a>	20	2	2.91	1.46	0.15	<a href="#">PTK2</a>
PATIENT_4	<a href="#">chr9:122755886-122995482</a>	89	2	2.92	1.46	0.24	--
PATIENT_4	<a href="#">chr10:119758595-120085826</a>	23	2	2.91	1.46	0.33	--
PATIENT_4	<a href="#">chr11:3834134-6869971</a>	677	2	2.92	1.46	3.04	<a href="#">ILK;RRM1</a>
PATIENT_4	<a href="#">chr11:17273506-17309528</a>	13	2	2.92	1.46	0.04	--
PATIENT_4	<a href="#">chr11:32565170-33700522</a>	184	2	2.91	1.46	1.14	<a href="#">HIPK3</a>
PATIENT_4	<a href="#">chr12:26431682-26639714</a>	25	2	2.92	1.46	0.21	--
PATIENT_4	<a href="#">chr13:32614469-34924282</a>	67	2	2.91	1.46	2.31	--
PATIENT_4	<a href="#">chr13:37035476-37832899</a>	44	2	2.93	1.46	0.8	--
PATIENT_4	<a href="#">chr14:36205452-36450928</a>	19	2	2.92	1.46	0.25	--
PATIENT_4	<a href="#">chr15:69907344-69976967</a>	17	2	2.92	1.46	0.07	--
PATIENT_4	<a href="#">chr1:155370588-156078098</a>	89	2	2.9	1.45	0.71	--
PATIENT_4	<a href="#">chr4:147781400-151631582</a>	125	2	2.91	1.45	3.85	--
PATIENT_4	<a href="#">chr5:145480171-145537361</a>	31	2	2.91	1.45	0.06	--
PATIENT_4	<a href="#">chr5:161512804-167457644</a>	49	2	2.89	1.45	5.94	--
PATIENT_4	<a href="#">chr5:168553092-170625448</a>	161	2	2.89	1.45	2.07	<a href="#">RANBP17</a>
PATIENT_4	<a href="#">chr6:81110130-82998208</a>	33	2	2.91	1.45	1.89	--

PATIENT_4	<a href="#">chr6:143116038-143813896</a>	50	2	2.89	1.45	0.7	--
PATIENT_4	<a href="#">chr6:169846059-169918012</a>	30	2	2.89	1.45	0.07	--
PATIENT_4	<a href="#">chr9:116595032-116884833</a>	40	2	2.9	1.45	0.29	--
PATIENT_4	<a href="#">chr15:97513931-98064514</a>	28	2	2.91	1.45	0.55	--
PATIENT_4	<a href="#">chr18:70622397-70761551</a>	7	2	2.91	1.45	0.14	--
PATIENT_4	<a href="#">chr21:32929039-33064028</a>	57	2	2.91	1.45	0.13	--
PATIENT_4	<a href="#">chrX:41331137-44087752</a>	76	2	2.9	1.45	2.76	<a href="#">CASK</a>
PATIENT_4	<a href="#">chrX:68757480-69166090</a>	14	2	2.89	1.45	0.41	--
PATIENT_4	<a href="#">chrX:87895306-96026736</a>	57	2	2.9	1.45	8.13	--
PATIENT_4	<a href="#">chr1:107492864-108530032</a>	48	2	2.88	1.44	1.04	--
PATIENT_4	<a href="#">chr1:169940276-170017798</a>	8	2	2.88	1.44	0.08	--
PATIENT_4	<a href="#">chr1:232586136-232809644</a>	32	2	2.87	1.44	0.22	--
PATIENT_4	<a href="#">chr1:238441077-240083336</a>	105	2	2.88	1.44	1.64	<a href="#">FH</a>
PATIENT_4	<a href="#">chr2:64177122-64717337</a>	31	2	2.89	1.44	0.54	--
PATIENT_4	<a href="#">chr2:132101144-132440668</a>	7	2	2.88	1.44	0.34	--
PATIENT_4	<a href="#">chr3:145049767-145191216</a>	7	2	2.89	1.44	0.14	--
PATIENT_4	<a href="#">chr4:52558760-53220044</a>	46	2	2.88	1.44	0.66	--
PATIENT_4	<a href="#">chr4:77100277-77576330</a>	108	2	2.89	1.44	0.48	--
PATIENT_4	<a href="#">chr4:99283264-100458292</a>	87	2	2.87	1.44	1.18	<a href="#">RAP1GDS1</a>
PATIENT_4	<a href="#">chr5:40945462-41185212</a>	62	2	2.88	1.44	0.24	--
PATIENT_4	<a href="#">chr5:52441286-53787646</a>	21	2	2.88	1.44	1.35	--
PATIENT_4	<a href="#">chr5:173270160-173467014</a>	18	2	2.88	1.44	0.2	--
PATIENT_4	<a href="#">chr6:52396842-52982258</a>	62	2	2.88	1.44	0.59	<a href="#">ICK</a>
PATIENT_4	<a href="#">chr6:127839020-127879278</a>	8	2	2.88	1.44	0.04	--
PATIENT_4	<a href="#">chr7:27532435-30454466</a>	137	2	2.88	1.44	2.92	<a href="#">JAZF1</a>
PATIENT_4	<a href="#">chr16:10434934-10482288</a>	8	2	2.88	1.44	0.05	--
PATIENT_4	<a href="#">chr17:59437749-59475976</a>	4	2	2.88	1.44	0.04	--
PATIENT_4	<a href="#">chr20:14255823-16299228</a>	22	2	2.88	1.44	2.04	--
PATIENT_4	<a href="#">chr20:31035349-31293961</a>	117	2	2.87	1.44	0.26	--
PATIENT_4	<a href="#">chrX:62774697-63322752</a>	12	2	2.89	1.44	0.55	--
PATIENT_4	<a href="#">chr1:166137870-166332408</a>	33	2	2.87	1.43	0.19	--
PATIENT_4	<a href="#">chr1:178524190-179119790</a>	47	2	2.87	1.43	0.6	--

PATIENT_4	<a href="#">chr1:198996762-199083402</a>	9	2	2.86	1.43	0.09	--
PATIENT_4	<a href="#">chr2:88638469-89866440</a>	130	2	2.86	1.43	1.23	<a href="#">EIF2AK3</a>
PATIENT_4	<a href="#">chr2:136381400-136457454</a>	15	2	2.85	1.43	0.08	--
PATIENT_4	<a href="#">chr2:201957124-202330456</a>	122	2	2.85	1.43	0.37	--
PATIENT_4	<a href="#">chr2:220214652-223221732</a>	61	2	2.86	1.43	3.01	EPHA4;PAX3
PATIENT_4	<a href="#">chr2:230749648-231390784</a>	100	2	2.86	1.43	0.64	--
PATIENT_4	<a href="#">chr2:231629984-231681618</a>	17	2	2.87	1.43	0.05	--
PATIENT_4	<a href="#">chr4:109085748-110003944</a>	70	2	2.87	1.43	0.92	--
PATIENT_4	<a href="#">chr4:151728730-152069166</a>	43	2	2.85	1.43	0.34	--
PATIENT_4	<a href="#">chr4:169610948-170254317</a>	39	2	2.86	1.43	0.64	--
PATIENT_4	<a href="#">chr6:44444148-44544193</a>	23	2	2.86	1.43	0.1	--
PATIENT_4	<a href="#">chr6:96160753-97076499</a>	9	2	2.86	1.43	0.92	--
PATIENT_4	<a href="#">chr7:140124301-142271546</a>	253	2	2.86	1.43	2.15	BRAF;EPHB6;FLJ40852
PATIENT_4	<a href="#">chr8:71234368-72274160</a>	33	2	2.85	1.43	1.04	--
PATIENT_4	<a href="#">chr8:95209688-95577824</a>	45	2	2.87	1.43	0.37	--
PATIENT_4	<a href="#">chr8:125037468-125412188</a>	49	2	2.86	1.43	0.37	--
PATIENT_4	<a href="#">chr9:67516685-70813179</a>	51	2	2.85	1.43	3.3	--
PATIENT_4	<a href="#">chr10:44105669-44120280</a>	4	2	2.85	1.43	0.01	--
PATIENT_4	<a href="#">chr10:90322716-90764012</a>	85	2	2.87	1.43	0.44	--
PATIENT_4	<a href="#">chr11:33752558-34110295</a>	35	2	2.86	1.43	0.36	<a href="#">LMO2</a>
PATIENT_4	<a href="#">chr12:77045084-81396875</a>	254	2	2.86	1.43	4.35	--
PATIENT_4	<a href="#">chr12:88517120-90096401</a>	56	2	2.85	1.43	1.58	--
PATIENT_4	<a href="#">chr20:33060170-33166956</a>	13	2	2.86	1.43	0.11	--
PATIENT_4	<a href="#">chrX:5821400-8960426</a>	67	2	2.86	1.43	3.14	--
PATIENT_4	<a href="#">chr1:74811642-75779720</a>	66	2	2.85	1.42	0.97	--
PATIENT_4	<a href="#">chr1:156936588-157078565</a>	25	2	2.83	1.42	0.14	--
PATIENT_4	<a href="#">chr2:74971496-75598730</a>	14	2	2.84	1.42	0.63	--
PATIENT_4	<a href="#">chr2:120283965-120767238</a>	58	2	2.84	1.42	0.48	--
PATIENT_4	<a href="#">chr2:127781740-127817155</a>	16	2	2.84	1.42	0.04	--
PATIENT_4	<a href="#">chr3:77609326-87078891</a>	90	2	2.85	1.42	9.47	--
PATIENT_4	<a href="#">chr4:85744482-90390177</a>	467	2	2.85	1.42	4.65	<a href="#">MAPK10</a>
PATIENT_4	<a href="#">chr4:146250788-147078980</a>	83	2	2.84	1.42	0.83	--

PATIENT_4	<a href="#">chr6:97353084-97669091</a>	19	2	2.85	1.42	0.32	--
PATIENT_4	<a href="#">chr7:14688768-14691450</a>	3	2	2.83	1.42	0	--
PATIENT_4	<a href="#">chr7:90734006-92603024</a>	272	2	2.85	1.42	1.87	AKAP9;CDK6
PATIENT_4	<a href="#">chr8:124762714-124858735</a>	16	2	2.85	1.42	0.1	--
PATIENT_4	<a href="#">chr9:13097032-14169736</a>	54	2	2.83	1.42	1.07	<a href="#">NFIB</a>
PATIENT_4	<a href="#">chr9:100095946-109131698</a>	512	2	2.84	1.42	9.04	NR4A3;TAL2;TGFBR1
PATIENT_4	<a href="#">chr11:55168708-55171934</a>	5	2	2.84	1.42	0	--
PATIENT_4	<a href="#">chr15:19072299-19073754</a>	2	2	2.84	1.42	0	--
PATIENT_4	<a href="#">chr15:30699626-30936548</a>	30	2	2.84	1.42	0.24	--
PATIENT_4	<a href="#">chr15:68155528-68781280</a>	40	2	2.84	1.42	0.63	--
PATIENT_4	<a href="#">chr15:71196068-71368580</a>	26	2	2.83	1.42	0.17	--
PATIENT_4	<a href="#">chr20:39221966-39467178</a>	86	2	2.83	1.42	0.25	--
PATIENT_4	<a href="#">chrX:47590610-47660154</a>	7	2	2.85	1.42	0.07	--
PATIENT_4	<a href="#">chr1:172174528-177152090</a>	294	2	2.83	1.41	4.98	--
PATIENT_4	<a href="#">chr1:211310975-212237928</a>	30	2	2.82	1.41	0.93	<a href="#">RPS6KC1</a>
PATIENT_4	<a href="#">chr1:212626844-212903652</a>	63	2	2.82	1.41	0.28	--
PATIENT_4	<a href="#">chr1:229904366-231007502</a>	50	2	2.83	1.41	1.1	--
PATIENT_4	<a href="#">chr2:148932849-152740378</a>	376	2	2.82	1.41	3.81	--
PATIENT_4	<a href="#">chr3:143175654-144163828</a>	160	2	2.81	1.41	0.99	<a href="#">ATR</a>
PATIENT_4	<a href="#">chr5:159730156-160653937</a>	61	2	2.81	1.41	0.92	--
PATIENT_4	<a href="#">chr6:22395690-24461777</a>	20	2	2.83	1.41	2.07	--
PATIENT_4	<a href="#">chr6:151901011-152688844</a>	93	2	2.81	1.41	0.79	<a href="#">ESR1</a>
PATIENT_4	<a href="#">chr7:68702708-69801497</a>	7	2	2.81	1.41	1.1	--
PATIENT_4	<a href="#">chr7:102189030-104534874</a>	219	2	2.82	1.41	2.35	--
PATIENT_4	<a href="#">chr7:151510122-151591106</a>	34	2	2.82	1.41	0.08	<a href="#">MLL3</a>
PATIENT_4	<a href="#">chr9:117989450-118420485</a>	36	2	2.83	1.41	0.43	--
PATIENT_4	<a href="#">chr11:57891620-57903355</a>	8	2	2.82	1.41	0.01	--
PATIENT_4	<a href="#">chr12:37000358-40247908</a>	189	2	2.81	1.41	3.25	<a href="#">LRRK2</a>
PATIENT_4	<a href="#">chr13:76593542-77375679</a>	104	2	2.82	1.41	0.78	--
PATIENT_4	<a href="#">chr17:55611471-55777674</a>	36	2	2.81	1.41	0.17	--
PATIENT_4	<a href="#">chrX:20089736-21302962</a>	21	2	2.83	1.41	1.21	<a href="#">RPS6KA3</a>
PATIENT_4	<a href="#">chrX:21796546-22929826</a>	54	2	2.81	1.41	1.13	--

PATIENT_4	<a href="#">chrX:49048334-50393298</a>	130	2	2.81	1.41	1.34	--
PATIENT_4	<a href="#">chrX:55058796-56293431</a>	71	2	2.81	1.41	1.23	--
PATIENT_4	<a href="#">chrX:63407612-64112956</a>	18	2	2.82	1.41	0.71	--
PATIENT_4	<a href="#">chrX:66682878-67411314</a>	31	2	2.81	1.41	0.73	<a href="#">AR</a>
PATIENT_4	<a href="#">chrX:114374785-114750850</a>	7	2	2.83	1.41	0.38	--
PATIENT_4	<a href="#">chr1:117746407-117867032</a>	13	2	2.81	1.4	0.12	--
PATIENT_4	<a href="#">chr2:120078798-120130450</a>	16	2	2.79	1.4	0.05	--
PATIENT_4	<a href="#">chr2:131697686-131737580</a>	6	2	2.8	1.4	0.04	--
PATIENT_4	<a href="#">chr2:227437851-228105128</a>	130	2	2.8	1.4	0.67	--
PATIENT_4	<a href="#">chr3:170974858-171009144</a>	20	2	2.81	1.4	0.03	--
PATIENT_4	<a href="#">chr4:159785612-162526938</a>	93	2	2.79	1.4	2.74	--
PATIENT_4	<a href="#">chr5:64894992-65386468</a>	90	2	2.8	1.4	0.49	--
PATIENT_4	<a href="#">chr5:74020976-76024972</a>	224	2	2.8	1.4	2	--
PATIENT_4	<a href="#">chr6:53246036-53517316</a>	23	2	2.79	1.4	0.27	--
PATIENT_4	<a href="#">chr7:105283268-105712534</a>	46	2	2.8	1.4	0.43	--
PATIENT_4	<a href="#">chr7:154724250-155260460</a>	34	2	2.79	1.4	0.54	--
PATIENT_4	<a href="#">chr8:70638852-70836593</a>	33	2	2.8	1.4	0.2	--
PATIENT_4	<a href="#">chr8:129042083-130960845</a>	27	2	2.8	1.4	1.92	--
PATIENT_4	<a href="#">chr11:17067956-17133704</a>	31	2	2.8	1.4	0.07	--
PATIENT_4	<a href="#">chr11:58236871-58649474</a>	27	2	2.8	1.4	0.41	--
PATIENT_4	<a href="#">chr16:12200996-12666357</a>	10	2	2.8	1.4	0.47	--
PATIENT_4	<a href="#">chr20:33752170-33852880</a>	19	2	2.81	1.4	0.1	--
PATIENT_4	<a href="#">chr20:41656810-41682960</a>	9	2	2.8	1.4	0.03	--
PATIENT_4	<a href="#">chr22:44464314-44618203</a>	11	2	2.8	1.4	0.15	--
PATIENT_4	<a href="#">chr1:233892913-234082946</a>	71	2	2.78	1.39	0.19	--
PATIENT_4	<a href="#">chr1:240495334-241500096</a>	33	2	2.77	1.39	1	--
PATIENT_4	<a href="#">chr2:132891819-133259208</a>	32	2	2.78	1.39	0.37	--
PATIENT_4	<a href="#">chr3:198255929-198508443</a>	26	2	2.77	1.39	0.25	--
PATIENT_4	<a href="#">chr4:103863159-104046244</a>	18	2	2.78	1.39	0.18	--
PATIENT_4	<a href="#">chr5:6544384-7573940</a>	39	2	2.79	1.39	1.03	--
PATIENT_4	<a href="#">chr5:40764256-40813363</a>	14	2	2.77	1.39	0.05	<a href="#">PRKAA1</a>
PATIENT_4	<a href="#">chr6:99481278-100163836</a>	70	2	2.78	1.39	0.68	--

PATIENT_4	<a href="#">chr6:136707054-137276319</a>	58	2	2.78	1.39	0.57	<a href="#">MAP3K5</a>
PATIENT_4	<a href="#">chr6:143866754-144300498</a>	39	2	2.78	1.39	0.43	--
PATIENT_4	<a href="#">chr6:150579680-150760965</a>	8	2	2.77	1.39	0.18	--
PATIENT_4	<a href="#">chr6:169599608-169830906</a>	29	2	2.78	1.39	0.23	--
PATIENT_4	<a href="#">chr7:20791814-26370717</a>	367	2	2.79	1.39	5.58	<a href="#">HNRNPA2B1;STK31</a>
PATIENT_4	<a href="#">chr7:149577043-149623282</a>	6	2	2.78	1.39	0.05	--
PATIENT_4	<a href="#">chr8:39121636-39813840</a>	69	2	2.79	1.39	0.69	--
PATIENT_4	<a href="#">chr8:57287984-59486526</a>	32	2	2.77	1.39	2.2	<a href="#">CHCHD7</a>
PATIENT_4	<a href="#">chr8:118881208-118918567</a>	10	2	2.79	1.39	0.04	<a href="#">EXT1</a>
PATIENT_4	<a href="#">chr9:112213709-113253576</a>	122	2	2.78	1.39	1.04	--
PATIENT_4	<a href="#">chr9:124759215-124836821</a>	13	2	2.78	1.39	0.08	--
PATIENT_4	<a href="#">chr11:16767300-17053705</a>	31	2	2.78	1.39	0.29	--
PATIENT_4	<a href="#">chr11:92521446-92767345</a>	21	2	2.77	1.39	0.25	--
PATIENT_4	<a href="#">chr12:13611334-13719995</a>	9	2	2.77	1.39	0.11	--
PATIENT_4	<a href="#">chr13:78089170-79023192</a>	37	2	2.78	1.39	0.93	--
PATIENT_4	<a href="#">chr15:32936476-33014090</a>	26	2	2.79	1.39	0.08	--
PATIENT_4	<a href="#">chr15:84488004-86956154</a>	69	2	2.78	1.39	2.47	<a href="#">NTRK3</a>
PATIENT_4	<a href="#">chr16:74869094-75149977</a>	25	2	2.78	1.39	0.28	--
PATIENT_4	<a href="#">chr17:45032789-45133840</a>	10	2	2.79	1.39	0.1	--
PATIENT_4	<a href="#">chr17:67629436-68592551</a>	14	2	2.79	1.39	0.96	--
PATIENT_4	<a href="#">chr18:17485606-19343206</a>	120	2	2.79	1.39	1.86	<a href="#">RIOK3</a>
PATIENT_4	<a href="#">chr18:37796524-40710607</a>	74	2	2.78	1.39	2.91	--
PATIENT_4	<a href="#">chr18:59611412-66023429</a>	171	2	2.78	1.39	6.41	--
PATIENT_4	<a href="#">chr20:31902465-32156888</a>	24	2	2.77	1.39	0.25	--
PATIENT_4	<a href="#">chr20:34954800-36550571</a>	220	2	2.78	1.39	1.6	<a href="#">SRC</a>
PATIENT_4	<a href="#">chrX:65155476-66681800</a>	38	2	2.78	1.39	1.53	<a href="#">AR</a>
PATIENT_4	<a href="#">chrX:78509304-79819506</a>	19	2	2.79	1.39	1.31	--
PATIENT_4	<a href="#">chrX:148384000-149389212</a>	62	2	2.79	1.39	1.01	--
PATIENT_4	<a href="#">chr1:95382128-99539948</a>	76	2	2.76	1.38	4.16	<a href="#">DPYD</a>
PATIENT_4	<a href="#">chr1:199088356-199093640</a>	6	2	2.76	1.38	0.01	--
PATIENT_4	<a href="#">chr2:202340259-202463800</a>	14	2	2.75	1.38	0.12	--
PATIENT_4	<a href="#">chr2:208738754-208903594</a>	44	2	2.75	1.38	0.16	<a href="#">IDH1</a>

PATIENT_4	<a href="#">chr2:228592372-230413840</a>	70	2	2.77	1.38	1.82	--
PATIENT_4	<a href="#">chr2:234054632-235069382</a>	128	2	2.76	1.38	1.01	<a href="#">UGT1A1</a>
PATIENT_4	<a href="#">chr3:135680176-137307793</a>	71	2	2.75	1.38	1.63	--
PATIENT_4	<a href="#">chr3:166388412-166390749</a>	15	2	2.75	1.38	0	--
PATIENT_4	<a href="#">chr4:96309456-96385210</a>	13	2	2.76	1.38	0.08	--
PATIENT_4	<a href="#">chr4:191099176-191185332</a>	23	2	2.75	1.38	0.09	--
PATIENT_4	<a href="#">chr7:20634900-20761646</a>	28	2	2.76	1.38	0.13	--
PATIENT_4	<a href="#">chr7:50435188-50767482</a>	43	2	2.77	1.38	0.33	--
PATIENT_4	<a href="#">chr8:102005353-103493606</a>	100	2	2.76	1.38	1.49	--
PATIENT_4	<a href="#">chr10:15864176-15929890</a>	13	2	2.75	1.38	0.07	--
PATIENT_4	<a href="#">chr10:91455100-92493374</a>	39	2	2.76	1.38	1.04	--
PATIENT_4	<a href="#">chr11:128351696-128567242</a>	19	2	2.76	1.38	0.22	--
PATIENT_4	<a href="#">chr12:20413529-22579490</a>	253	2	2.75	1.38	2.17	--
PATIENT_4	<a href="#">chr20:32428916-32760258</a>	54	2	2.76	1.38	0.33	--
PATIENT_4	<a href="#">chr20:42008008-42309460</a>	26	2	2.76	1.38	0.3	--
PATIENT_4	<a href="#">chr21:29177197-31520031</a>	197	2	2.75	1.38	2.34	--
PATIENT_4	<a href="#">chr1:178221962-178346810</a>	57	2	2.74	1.37	0.12	--
PATIENT_4	<a href="#">chr1:180724078-183541336</a>	337	2	2.73	1.37	2.82	<a href="#">RNASEL</a>
PATIENT_4	<a href="#">chr1:200652596-200804898</a>	23	2	2.73	1.37	0.15	--
PATIENT_4	<a href="#">chr3:28279842-31652517</a>	79	2	2.73	1.37	3.37	<a href="#">TGFBR2</a>
PATIENT_4	<a href="#">chr3:55959572-56305238</a>	11	2	2.74	1.37	0.35	--
PATIENT_4	<a href="#">chr3:195608006-195664177</a>	32	2	2.75	1.37	0.06	--
PATIENT_4	<a href="#">chr5:50126548-50126876</a>	3	2	2.73	1.37	0	--
PATIENT_4	<a href="#">chr5:126168434-126411360</a>	16	2	2.75	1.37	0.24	--
PATIENT_4	<a href="#">chr6:159379199-159573262</a>	21	2	2.73	1.37	0.19	--
PATIENT_4	<a href="#">chr7:54577952-55466450</a>	46	2	2.74	1.37	0.89	<a href="#">EGFR</a>
PATIENT_4	<a href="#">chr7:76709058-76873314</a>	48	2	2.74	1.37	0.16	--
PATIENT_4	<a href="#">chr7:94123280-94588027</a>	19	2	2.74	1.37	0.46	--
PATIENT_4	<a href="#">chr8:24207634-24421938</a>	59	2	2.73	1.37	0.21	--
PATIENT_4	<a href="#">chr9:89532384-89591546</a>	12	2	2.75	1.37	0.06	--
PATIENT_4	<a href="#">chr9:113449281-113593490</a>	41	2	2.74	1.37	0.14	--
PATIENT_4	<a href="#">chr11:100504920-100867582</a>	13	2	2.74	1.37	0.36	<a href="#">PGR</a>

PATIENT_4	<a href="#">chr12:14833201-18781564</a>	188	2	2.74	1.37	3.95	--
PATIENT_4	<a href="#">chr12:95606870-96481750</a>	37	2	2.74	1.37	0.87	--
PATIENT_4	<a href="#">chr13:52501090-52515303</a>	4	2	2.74	1.37	0.01	--
PATIENT_4	<a href="#">chr14:93712168-93822277</a>	28	2	2.75	1.37	0.11	--
PATIENT_4	<a href="#">chr15:69978071-69980645</a>	4	2	2.75	1.37	0	--
PATIENT_4	<a href="#">chr15:81727930-82948227</a>	51	2	2.73	1.37	1.22	--
PATIENT_4	<a href="#">chr17:70428138-70480305</a>	44	2	2.73	1.37	0.05	--
PATIENT_4	<a href="#">chr20:54012438-54373627</a>	9	2	2.74	1.37	0.36	--
PATIENT_4	<a href="#">chr1:115199644-115404640</a>	42	2	2.71	1.36	0.2	--
PATIENT_4	<a href="#">chr1:150114010-150327163</a>	23	2	2.73	1.36	0.21	--
PATIENT_4	<a href="#">chr1:150460132-150541876</a>	4	2	2.72	1.36	0.08	--
PATIENT_4	<a href="#">chr1:212545172-212623430</a>	18	2	2.73	1.36	0.08	--
PATIENT_4	<a href="#">chr2:206289242-206365222</a>	18	2	2.72	1.36	0.08	--
PATIENT_4	<a href="#">chr3:188450765-190074889</a>	44	2	2.71	1.36	1.62	BCL6;LPP
PATIENT_4	<a href="#">chr4:26225173-26619186</a>	32	2	2.72	1.36	0.39	--
PATIENT_4	<a href="#">chr4:110613688-111617426</a>	111	2	2.71	1.36	1	--
PATIENT_4	<a href="#">chr5:50719198-52133364</a>	10	2	2.73	1.36	1.41	--
PATIENT_4	<a href="#">chr5:134698634-137382601</a>	177	2	2.72	1.36	2.68	--
PATIENT_4	<a href="#">chr6:46933950-46935212</a>	8	2	2.73	1.36	0	--
PATIENT_4	<a href="#">chr6:159318675-159334879</a>	8	2	2.71	1.36	0.02	--
PATIENT_4	<a href="#">chr7:38336546-38400326</a>	19	2	2.73	1.36	0.06	--
PATIENT_4	<a href="#">chr7:152741002-154421342</a>	57	2	2.73	1.36	1.68	--
PATIENT_4	<a href="#">chr11:58075170-58140802</a>	15	2	2.72	1.36	0.07	--
PATIENT_4	<a href="#">chr11:94501772-95261013</a>	48	2	2.72	1.36	0.76	--
PATIENT_4	<a href="#">chr11:109958292-110000136</a>	11	2	2.73	1.36	0.04	--
PATIENT_4	<a href="#">chr13:95236252-96282766</a>	47	2	2.72	1.36	1.05	--
PATIENT_4	<a href="#">chr15:36639400-37673640</a>	29	2	2.72	1.36	1.03	--
PATIENT_4	<a href="#">chr16:31529540-33555286</a>	28	2	2.71	1.36	2.03	--
PATIENT_4	<a href="#">chr18:22751182-27180041</a>	94	2	2.71	1.36	4.43	--
PATIENT_4	<a href="#">chrX:44705533-46194840</a>	41	2	2.72	1.36	1.49	KDM6A
PATIENT_4	<a href="#">chrX:138736596-146801402</a>	130	2	2.72	1.36	8.06	--
PATIENT_4	<a href="#">chr1:207669320-208178226</a>	89	2	2.71	1.35	0.51	CAMK1G

PATIENT_4	<a href="#">chr1:218155567-220989472</a>	259	2	2.69	1.35	2.83	<a href="#">MARK1</a>
PATIENT_4	<a href="#">chr1:231008502-231581427</a>	69	2	2.7	1.35	0.57	<a href="#">KIAA1804</a>
PATIENT_4	<a href="#">chr2:16597720-17826638</a>	83	2	2.69	1.35	1.23	--
PATIENT_4	<a href="#">chr2:106054762-107809924</a>	44	2	2.7	1.35	1.76	--
PATIENT_4	<a href="#">chr2:163403217-164176398</a>	13	2	2.69	1.35	0.77	--
PATIENT_4	<a href="#">chr2:171558624-174909214</a>	265	2	2.71	1.35	3.35	PDK1;TLK1;ZAK
PATIENT_4	<a href="#">chr3:336500-3191896</a>	98	2	2.7	1.35	2.86	--
PATIENT_4	<a href="#">chr4:12979314-13207846</a>	27	2	2.7	1.35	0.23	--
PATIENT_4	<a href="#">chr4:53424208-53913600</a>	13	2	2.7	1.35	0.49	--
PATIENT_4	<a href="#">chr4:73633172-74224733</a>	43	2	2.71	1.35	0.59	--
PATIENT_4	<a href="#">chr4:111758882-113744208</a>	75	2	2.71	1.35	1.99	<a href="#">ALPK1</a>
PATIENT_4	<a href="#">chr5:70373806-72463220</a>	209	2	2.71	1.35	2.09	--
PATIENT_4	<a href="#">chr6:3977378-6599813</a>	111	2	2.7	1.35	2.62	<a href="#">PRPF4B</a>
PATIENT_4	<a href="#">chr7:99083908-99311654</a>	54	2	2.7	1.35	0.23	--
PATIENT_4	<a href="#">chr8:133948456-135739057</a>	117	2	2.7	1.35	1.79	--
PATIENT_4	<a href="#">chr9:2794395-3927108</a>	42	2	2.7	1.35	1.13	--
PATIENT_4	<a href="#">chr9:96575188-97051318</a>	36	2	2.7	1.35	0.48	<a href="#">FANCC</a>
PATIENT_4	<a href="#">chr10:92624612-93262067</a>	49	2	2.7	1.35	0.64	--
PATIENT_4	<a href="#">chr11:121475725-121528184</a>	4	2	2.7	1.35	0.05	--
PATIENT_4	<a href="#">chr13:38489630-39725276</a>	50	2	2.71	1.35	1.24	<a href="#">LHFP</a>
PATIENT_4	<a href="#">chr14:87512505-87524263</a>	5	2	2.69	1.35	0.01	--
PATIENT_4	<a href="#">chr15:37880632-38117822</a>	51	2	2.69	1.35	0.24	<a href="#">EIF2AK4</a>
PATIENT_4	<a href="#">chr15:50294126-50868466</a>	102	2	2.69	1.35	0.57	--
PATIENT_4	<a href="#">chr15:65249965-65886082</a>	67	2	2.7	1.35	0.64	<a href="#">MAP2K5</a>
PATIENT_4	<a href="#">chr15:89596140-91359013</a>	75	2	2.69	1.35	1.76	--
PATIENT_4	<a href="#">chr17:49255555-49256688</a>	6	2	2.7	1.35	0	--
PATIENT_4	<a href="#">chr17:71662956-71720085</a>	15	2	2.7	1.35	0.06	--
PATIENT_4	<a href="#">chr18:43622244-43650874</a>	9	2	2.7	1.35	0.03	--
PATIENT_4	<a href="#">chr20:60424635-61427250</a>	214	2	2.69	1.35	1	--
PATIENT_4	<a href="#">chr21:25900638-27218466</a>	64	2	2.69	1.35	1.32	--
PATIENT_4	<a href="#">chrX:23320574-23322172</a>	11	2	2.7	1.35	0	--
PATIENT_4	<a href="#">chr1:71091118-71250646</a>	9	2	2.69	1.34	0.16	--
PATIENT_4	<a href="#">chr1:165105668-165225630</a>	18	2	2.69	1.34	0.12	--
PATIENT_4	<a href="#">chr2:31599-659788</a>	33	2	2.67	1.34	0.63	--

PATIENT_4	<a href="#">chr2:108277164-108741342</a>	67	2	2.69	1.34	0.46	--
PATIENT_4	<a href="#">chr2:238159452-238407712</a>	49	2	2.68	1.34	0.25	--
PATIENT_4	<a href="#">chr3:122844478-123483705</a>	137	2	2.68	1.34	0.64	--
PATIENT_4	<a href="#">chr4:71235789-71751026</a>	66	2	2.68	1.34	0.52	--
PATIENT_4	<a href="#">chr4:104338896-106416880</a>	42	2	2.69	1.34	2.08	<a href="#">TET2</a>
PATIENT_4	<a href="#">chr4:114494644-114496350</a>	10	2	2.68	1.34	0	--
PATIENT_4	<a href="#">chr8:43271358-48515488</a>	22	2	2.68	1.34	5.24	--
PATIENT_4	<a href="#">chr8:94782050-94896783</a>	56	2	2.67	1.34	0.11	--
PATIENT_4	<a href="#">chr10:83224-278014</a>	14	2	2.68	1.34	0.19	--
PATIENT_4	<a href="#">chr11:48088190-48242874</a>	40	2	2.68	1.34	0.15	--
PATIENT_4	<a href="#">chr11:103413551-106936772</a>	129	2	2.68	1.34	3.52	--
PATIENT_4	<a href="#">chr12:22688080-24256651</a>	26	2	2.67	1.34	1.57	--
PATIENT_4	<a href="#">chr15:38249574-38300142</a>	23	2	2.67	1.34	0.05	BUB1B;PAK6
PATIENT_4	<a href="#">chr15:73933822-75028549</a>	96	2	2.67	1.34	1.09	--
PATIENT_4	<a href="#">chr16:13946112-14246961</a>	12	2	2.68	1.34	0.3	<a href="#">ERCC4</a>
PATIENT_4	<a href="#">chr17:46128422-46182938</a>	17	2	2.69	1.34	0.05	--
PATIENT_4	<a href="#">chr17:59144546-59246708</a>	34	2	2.67	1.34	0.1	--
PATIENT_4	<a href="#">chr17:71013275-71147934</a>	64	2	2.69	1.34	0.13	--
PATIENT_4	<a href="#">chr20:31625693-31691892</a>	10	2	2.67	1.34	0.07	--
PATIENT_4	<a href="#">chr22:28819968-28902095</a>	10	2	2.68	1.34	0.08	--
PATIENT_4	<a href="#">chrX:100868827-101892166</a>	110	2	2.69	1.34	1.02	--
PATIENT_4	<a href="#">chrX:119095026-119575864</a>	64	2	2.68	1.34	0.48	--
PATIENT_4	<a href="#">chr1:94415802-94778456</a>	54	2	2.66	1.33	0.36	--
PATIENT_4	<a href="#">chr1:144480798-145598440</a>	87	2	2.66	1.33	1.12	<a href="#">BCL9</a>
PATIENT_4	<a href="#">chr1:156491536-156843407</a>	70	2	2.67	1.33	0.35	--
PATIENT_4	<a href="#">chr2:74144138-74167618</a>	10	2	2.67	1.33	0.02	--
PATIENT_4	<a href="#">chr2:178124178-178202443</a>	23	2	2.66	1.33	0.08	--
PATIENT_4	<a href="#">chr2:239823238-240610332</a>	18	2	2.66	1.33	0.79	--
PATIENT_4	<a href="#">chr4:141708378-142108354</a>	34	2	2.67	1.33	0.4	--
PATIENT_4	<a href="#">chr5:56213356-56814268</a>	50	2	2.66	1.33	0.6	<a href="#">MAP3K1</a>
PATIENT_4	<a href="#">chr5:115810274-115831264</a>	8	2	2.66	1.33	0.02	--
PATIENT_4	<a href="#">chr5:171228340-171273976</a>	11	2	2.67	1.33	0.05	--

PATIENT_4	<a href="#">chr6:47757104-47758274</a>	7	2	2.66	1.33	0	--
PATIENT_4	<a href="#">chr8:72917486-72918726</a>	3	2	2.66	1.33	0	--
PATIENT_4	<a href="#">chr8:139222696-139925546</a>	87	2	2.65	1.33	0.7	--
PATIENT_4	<a href="#">chr9:17133311-18765780</a>	68	2	2.66	1.33	1.63	--
PATIENT_4	<a href="#">chr9:110671248-111938497</a>	150	2	2.67	1.33	1.27	--
PATIENT_4	<a href="#">chr10:112626468-112754436</a>	19	2	2.66	1.33	0.13	--
PATIENT_4	<a href="#">chr11:8452801-9044063</a>	104	2	2.66	1.33	0.59	<a href="#">STK33</a>
PATIENT_4	<a href="#">chr11:17375858-17757660</a>	76	2	2.66	1.33	0.38	--
PATIENT_4	<a href="#">chr11:95726478-100502009</a>	83	2	2.65	1.33	4.78	<a href="#">PGR</a>
PATIENT_4	<a href="#">chr11:101899256-103376192</a>	199	2	2.66	1.33	1.48	--
PATIENT_4	<a href="#">chr13:75038912-75330102</a>	46	2	2.66	1.33	0.29	--
PATIENT_4	<a href="#">chr14:24351764-28306290</a>	16	2	2.65	1.33	3.95	--
PATIENT_4	<a href="#">chr14:96369626-96417270</a>	12	2	2.66	1.33	0.05	<a href="#">VRK1</a>
PATIENT_4	<a href="#">chr17:70979586-71011375</a>	46	2	2.66	1.33	0.03	--
PATIENT_4	<a href="#">chr20:54405752-55338400</a>	61	2	2.67	1.33	0.93	--
PATIENT_4	<a href="#">chrX:54978136-55046970</a>	17	2	2.66	1.33	0.07	--
PATIENT_4	<a href="#">chr2:119316994-119468483</a>	21	2	2.65	1.32	0.15	--
PATIENT_4	<a href="#">chr2:169858964-171217801</a>	184	2	2.63	1.32	1.36	<a href="#">MYO3B</a>
PATIENT_4	<a href="#">chr2:182229842-182465619</a>	10	2	2.64	1.32	0.24	--
PATIENT_4	<a href="#">chr3:16311430-19550340</a>	95	2	2.65	1.32	3.24	--
PATIENT_4	<a href="#">chr3:45842792-45850746</a>	7	2	2.65	1.32	0.01	--
PATIENT_4	<a href="#">chr3:116877537-122786520</a>	309	2	2.65	1.32	5.91	<a href="#">GSK3B</a>
PATIENT_4	<a href="#">chr3:194715246-194815470</a>	6	2	2.64	1.32	0.1	--
PATIENT_4	<a href="#">chr4:144836262-144840108</a>	21	2	2.65	1.32	0	--
PATIENT_4	<a href="#">chr4:164466294-164466874</a>	3	2	2.64	1.32	0	--
PATIENT_4	<a href="#">chr5:108726500-108745138</a>	9	2	2.64	1.32	0.02	--
PATIENT_4	<a href="#">chr6:159575096-16306877</a>	282	2	2.63	1.32	3.49	<a href="#">MAP3K4</a>
PATIENT_4	<a href="#">chr7:40280708-43450553</a>	70	2	2.64	1.32	3.17	--
PATIENT_4	<a href="#">chr8:13207160-17188264</a>	90	2	2.64	1.32	3.98	--
PATIENT_4	<a href="#">chr8:120497986-120934552</a>	71	2	2.65	1.32	0.44	--
PATIENT_4	<a href="#">chr9:6870021-12699070</a>	70	2	2.64	1.32	5.83	--
PATIENT_4	<a href="#">chr10:124142766-124176488</a>	10	2	2.64	1.32	0.03	--
PATIENT_4	<a href="#">chr12:46343576-46382788</a>	16	2	2.65	1.32	0.04	--

PATIENT_4	<a href="#">chr13:50827216-50924590</a>	22	2	2.65	1.32	0.1	--
PATIENT_4	<a href="#">chr16:54094239-54174416</a>	20	2	2.65	1.32	0.08	--
PATIENT_4	<a href="#">chr17:55863356-55926660</a>	12	2	2.63	1.32	0.06	--
PATIENT_4	<a href="#">chr17:71235114-71438918</a>	160	2	2.63	1.32	0.2	--
PATIENT_4	<a href="#">chr17:71580046-71611324</a>	40	2	2.65	1.32	0.03	--
PATIENT_4	<a href="#">chr18:9327288-9389420</a>	5	2	2.65	1.32	0.06	--
PATIENT_4	<a href="#">chr20:36643349-37024437</a>	57	2	2.65	1.32	0.38	--
PATIENT_4	<a href="#">chr20:58316978-60315147</a>	98	2	2.64	1.32	2	<a href="#">SS18L1</a>
PATIENT_4	<a href="#">chr22:24291066-24447298</a>	20	2	2.65	1.32	0.16	<a href="#">ADRBK2</a>
PATIENT_4	<a href="#">chrX:24422832-30782143</a>	174	2	2.63	1.32	6.36	<a href="#">PDK3</a>
PATIENT_4	<a href="#">chrX:122486894-122674424</a>	42	2	2.65	1.32	0.19	--
PATIENT_4	<a href="#">chr2:45470032-46091046</a>	32	2	2.63	1.31	0.62	<a href="#">PRKCE</a>
PATIENT_4	<a href="#">chr2:109730537-112959994</a>	217	2	2.61	1.31	3.23	BUB1;MERTK;TTL
PATIENT_4	<a href="#">chr3:8898080-8975628</a>	12	2	2.62	1.31	0.08	--
PATIENT_4	<a href="#">chr5:54588071-55564462</a>	149	2	2.62	1.31	0.98	<a href="#">IL6ST</a>
PATIENT_4	<a href="#">chr5:68911380-70283541</a>	9	2	2.61	1.31	1.37	--
PATIENT_4	<a href="#">chr5:118352029-118541701</a>	41	2	2.63	1.31	0.19	--
PATIENT_4	<a href="#">chr6:27987874-28987438</a>	153	2	2.62	1.31	1	<a href="#">TRIM27</a>
PATIENT_4	<a href="#">chr6:47789870-47790744</a>	5	2	2.62	1.31	0	--
PATIENT_4	<a href="#">chr6:52121778-52319480</a>	26	2	2.62	1.31	0.2	--
PATIENT_4	<a href="#">chr6:105284266-107338733</a>	131	2	2.63	1.31	2.05	<a href="#">PRDM1</a>
PATIENT_4	<a href="#">chr7:17946427-18033862</a>	8	2	2.62	1.31	0.09	--
PATIENT_4	<a href="#">chr7:43457013-43777268</a>	31	2	2.62	1.31	0.32	<a href="#">STK17A</a>
PATIENT_4	<a href="#">chr8:73150142-75426156</a>	96	2	2.62	1.31	2.28	--
PATIENT_4	<a href="#">chr10:20330825-21349082</a>	43	2	2.62	1.31	1.02	--
PATIENT_4	<a href="#">chr11:67682974-67714024</a>	11	2	2.63	1.31	0.03	--
PATIENT_4	<a href="#">chr12:44614516-45473077</a>	52	2	2.61	1.31	0.86	--
PATIENT_4	<a href="#">chr13:76467291-76569734</a>	40	2	2.63	1.31	0.1	--
PATIENT_4	<a href="#">chr15:70031214-70125831</a>	16	2	2.62	1.31	0.09	--
PATIENT_4	<a href="#">chr20:29309166-29524468</a>	17	2	2.61	1.31	0.22	--
PATIENT_4	<a href="#">chrX:69637504-69943318</a>	24	2	2.62	1.31	0.31	--
PATIENT_4	<a href="#">chrX:85290312-85290743</a>	4	2	2.62	1.31	0	--
PATIENT_4	<a href="#">chrX:131920222-131989859</a>	13	2	2.61	1.31	0.07	--

PATIENT_4	<a href="#">chr2:177788506-177837525</a>	21	2	2.61	1.3	0.05	<a href="#">NFE2L2</a>
PATIENT_4	<a href="#">chr2:237908043-238125754</a>	76	2	2.6	1.3	0.22	--
PATIENT_4	<a href="#">chr3:156681436-157042996</a>	46	2	2.6	1.3	0.36	--
PATIENT_4	<a href="#">chr4:17434406-24143678</a>	144	2	2.6	1.3	6.71	--
PATIENT_4	<a href="#">chr9:111940589-112206537</a>	29	2	2.6	1.3	0.27	--
PATIENT_4	<a href="#">chr10:90964666-91051860</a>	10	2	2.6	1.3	0.09	--
PATIENT_4	<a href="#">chr15:23520186-24799446</a>	28	2	2.61	1.3	1.28	--
PATIENT_4	<a href="#">chr15:75258756-75558636</a>	23	2	2.6	1.3	0.3	--
PATIENT_4	<a href="#">chr22:34470200-34664862</a>	14	2	2.6	1.3	0.19	--
PATIENT_4	<a href="#">chrX:122984180-123384033</a>	56	2	2.6	1.3	0.4	--
PATIENT_4	<a href="#">chrX:153559700-154428029</a>	128	2	2.61	1.3	0.87	<a href="#">MTCP1</a>

#### Copy Number Losses in Patient 4

Sample	Region (hg18)	Number of Exons	Reference Number of Copies	Estimated Copy Number	Copy Number Ratio	Length of Containing Segment	Informative Genes in Region
PATIENT_4	<a href="#">chr19:50347176-50347669</a>	3	2	0.61	0.31	0	--
PATIENT_4	<a href="#">chr11:62302089-62302956</a>	3	2	0.72	0.36	0	--
PATIENT_4	<a href="#">chr19:3928266-3935223</a>	13	2	0.72	0.36	0.01	--
PATIENT_4	<a href="#">chr12:119503323-119503512</a>	3	2	0.76	0.38	0	--
PATIENT_4	<a href="#">chr19:59004821-59069506</a>	17	2	0.77	0.38	0.06	--
PATIENT_4	<a href="#">chr12:120563349-120591705</a>	7	2	0.78	0.39	0.03	--
PATIENT_4	<a href="#">chr12:122536188-122635219</a>	6	2	0.81	0.41	0.1	--
PATIENT_4	<a href="#">chr14:22414622-22415368</a>	5	2	0.83	0.41	0	--
PATIENT_4	<a href="#">chr19:52911730-53034578</a>	37	2	0.86	0.43	0.12	--
PATIENT_4	<a href="#">chr3:47863213-47871786</a>	20	2	0.9	0.45	0.01	--
PATIENT_4	<a href="#">chr14:22380592-22382392</a>	5	2	0.9	0.45	0	--
PATIENT_4	<a href="#">chr14:73893345-73944070</a>	13	2	0.91	0.45	0.05	--
PATIENT_4	<a href="#">chr19:34856631-34856988</a>	3	2	0.9	0.45	0	--
PATIENT_4	<a href="#">chr16:55973720-55974190</a>	4	2	0.92	0.46	0	--
PATIENT_4	<a href="#">chr16:74055930-74121592</a>	12	2	0.92	0.46	0.07	--
PATIENT_4	<a href="#">chr4:39124368-39125072</a>	6	2	0.95	0.47	0	--
PATIENT_4	<a href="#">chr10:105193733-105208142</a>	10	2	0.94	0.47	0.01	--
PATIENT_4	<a href="#">chr10:103815807-103859720</a>	14	2	0.97	0.48	0.04	--
PATIENT_4	<a href="#">chr11:62412524-62435085</a>	11	2	0.95	0.48	0.02	--

PATIENT_4	<a href="#">chr12:49031612-49034359</a>	16	2	0.96	0.48	0	--
PATIENT_4	<a href="#">chr12:121752782-121780746</a>	20	2	0.95	0.48	0.03	--
PATIENT_4	<a href="#">chr16:66236664-66255394</a>	66	2	0.95	0.48	0.02	--
PATIENT_4	<a href="#">chr17:2540722-2755364</a>	31	2	0.97	0.48	0.21	--
PATIENT_4	<a href="#">chr2:25954556-26111032</a>	18	2	0.98	0.49	0.16	--
PATIENT_4	<a href="#">chr9:33912560-33915852</a>	10	2	0.98	0.49	0	--
PATIENT_4	<a href="#">chr10:99110324-99129450</a>	19	2	0.97	0.49	0.02	--
PATIENT_4	<a href="#">chr16:31248672-31249166</a>	3	2	0.97	0.49	0	--
PATIENT_4	<a href="#">chr2:27452254-27456470</a>	10	2	1	0.5	0	--
PATIENT_4	<a href="#">chr11:77405408-77453007</a>	8	2	1	0.5	0.05	--
PATIENT_4	<a href="#">chr14:73037089-73128868</a>	23	2	1	0.5	0.09	--
PATIENT_4	<a href="#">chr14:101575212-101583940</a>	14	2	1.01	0.5	0.01	--
PATIENT_4	<a href="#">chr18:12315190-12316035</a>	7	2	1.01	0.5	0	--
PATIENT_4	<a href="#">chr19:3045702-3927634</a>	252	2	1.01	0.5	0.88	DAPK3;GNA11;MATK
PATIENT_4	<a href="#">chr19:3936386-5961197</a>	591	2	1.01	0.5	2.02	MAP2K2;SH3GL1
PATIENT_4	<a href="#">chr19:50350939-51067297</a>	288	2	1.01	0.5	0.72	DMPK;ERCC1;ERCC2;MARK4
PATIENT_4	<a href="#">chr2:24093270-24100536</a>	10	2	1.02	0.51	0.01	--
PATIENT_4	<a href="#">chr5:179038234-179038608</a>	3	2	1.01	0.51	0	--
PATIENT_4	<a href="#">chr10:99195533-99202650</a>	7	2	1.03	0.51	0.01	--
PATIENT_4	<a href="#">chr14:93475209-93475624</a>	3	2	1.02	0.51	0	--
PATIENT_4	<a href="#">chr16:66259126-66714380</a>	214	2	1.01	0.51	0.46	<a href="#">PSKH1</a>
PATIENT_4	<a href="#">chr17:587932-1893015</a>	341	2	1.02	0.51	1.31	--
PATIENT_4	<a href="#">chr18:42797214-42803185</a>	5	2	1.02	0.51	0.01	--
PATIENT_4	<a href="#">chr22:39405563-39407598</a>	5	2	1.03	0.51	0	--
PATIENT_4	<a href="#">chr2:233607448-233607668</a>	3	2	1.04	0.52	0	--
PATIENT_4	<a href="#">chr9:36159712-36160970</a>	7	2	1.03	0.52	0	--
PATIENT_4	<a href="#">chr16:70380752-70456374</a>	20	2	1.04	0.52	0.08	--
PATIENT_4	<a href="#">chr17:4395121-4878568</a>	327	2	1.04	0.52	0.48	--
PATIENT_4	<a href="#">chr19:43067827-44386688</a>	517	2	1.04	0.52	1.32	MAP4K1;PAK4
PATIENT_4	<a href="#">chr19:51542250-52897464</a>	325	2	1.04	0.52	1.36	<a href="#">PRKD2</a>
PATIENT_4	<a href="#">chr19:53034816-53338948</a>	60	2	1.04	0.52	0.3	--
PATIENT_4	<a href="#">chr7:65185323-65195251</a>	13	2	1.07	0.53	0.01	--
PATIENT_4	<a href="#">chr7:148356380-148399562</a>	7	2	1.06	0.53	0.04	--
PATIENT_4	<a href="#">chr12:116957234-117066856</a>	24	2	1.06	0.53	0.11	--

PATIENT_4	<a href="#">chr12:120635229-121276490</a>	142	2	1.07	0.53	0.64	<a href="#">BCL7A</a>
PATIENT_4	<a href="#">chr16:82785234-82886140</a>	20	2	1.06	0.53	0.1	--
PATIENT_4	<a href="#">chr17:3378954-3668410</a>	108	2	1.05	0.53	0.29	<a href="#">GSG2</a>
PATIENT_4	<a href="#">chr19:49712964-50347036</a>	163	2	1.06	0.53	0.63	BCL3;CBLC
PATIENT_4	<a href="#">chr19:53492108-56212488</a>	1171	2	1.06	0.53	2.72	KLK2;VRK3
PATIENT_4	<a href="#">chr19:58764448-59002638</a>	73	2	1.07	0.53	0.24	<a href="#">ZNF331</a>
PATIENT_4	<a href="#">chrX:44588358-44618138</a>	6	2	1.05	0.53	0.03	<a href="#">KDM6A</a>
PATIENT_4	<a href="#">chr3:32834674-32970516</a>	12	2	1.07	0.54	0.14	--
PATIENT_4	<a href="#">chr3:57517133-57520728</a>	8	2	1.08	0.54	0	--
PATIENT_4	<a href="#">chr4:39921434-40135373</a>	18	2	1.07	0.54	0.21	--
PATIENT_4	<a href="#">chr10:12110958-12200829</a>	20	2	1.09	0.54	0.09	--
PATIENT_4	<a href="#">chr19:61741-2979333</a>	999	2	1.07	0.54	2.92	CSNK1G2;FSTL3;MKNK2;TCF3
PATIENT_4	<a href="#">chr19:40126899-41730245</a>	676	2	1.09	0.54	1.6	--
PATIENT_4	<a href="#">chr19:45389896-46636104</a>	425	2	1.09	0.54	1.25	ADCK4;AKT2;AXL;HIPK4;MAP3K10
PATIENT_4	<a href="#">chr22:40408302-40425580</a>	6	2	1.08	0.54	0.02	--
PATIENT_4	<a href="#">chr1:45565820-45586183</a>	42	2	1.1	0.55	0.02	MUTYH;TESK2
PATIENT_4	<a href="#">chr1:45733361-45822430</a>	26	2	1.11	0.55	0.09	--
PATIENT_4	<a href="#">chr3:33109432-33110229</a>	6	2	1.09	0.55	0	--
PATIENT_4	<a href="#">chr7:5507516-5630241</a>	25	2	1.11	0.55	0.12	--
PATIENT_4	<a href="#">chr7:148418640-148433192</a>	9	2	1.09	0.55	0.01	--
PATIENT_4	<a href="#">chr9:34079490-34253132</a>	38	2	1.09	0.55	0.17	--
PATIENT_4	<a href="#">chr11:553220-553601</a>	4	2	1.1	0.55	0	--
PATIENT_4	<a href="#">chr12:1546198-1625522</a>	11	2	1.1	0.55	0.08	--
PATIENT_4	<a href="#">chr12:110226442-110379457</a>	37	2	1.1	0.55	0.15	--
PATIENT_4	<a href="#">chr12:119900954-120549252</a>	129	2	1.11	0.55	0.65	<a href="#">CAMKK2</a>
PATIENT_4	<a href="#">chr12:123914136-124153224</a>	46	2	1.11	0.55	0.24	--
PATIENT_4	<a href="#">chr13:97626670-97627426</a>	5	2	1.11	0.55	0	--
PATIENT_4	<a href="#">chr14:77005245-77048424</a>	8	2	1.1	0.55	0.04	--
PATIENT_4	<a href="#">chr16:57258812-57300892</a>	13	2	1.1	0.55	0.04	--
PATIENT_4	<a href="#">chr16:65981628-66202607</a>	60	2	1.1	0.55	0.22	--
PATIENT_4	<a href="#">chr16:82770363-82775998</a>	16	2	1.11	0.55	0.01	--
PATIENT_4	<a href="#">chr17:3715990-3800768</a>	46	2	1.1	0.55	0.08	<a href="#">CAMKK1</a>
PATIENT_4	<a href="#">chr17:4284088-4393158</a>	33	2	1.1	0.55	0.11	--
PATIENT_4	<a href="#">chr17:27838859-27845956</a>	6	2	1.11	0.55	0.01	--
PATIENT_4	<a href="#">chr19:42368088-42571404</a>	35	2	1.11	0.55	0.2	--

PATIENT_4	<a href="#">chr19:60434635-60782078</a>	160	2	1.1	0.55	0.35	<a href="#">BRSK1</a>
PATIENT_4	<a href="#">chrX:118711080-118777480</a>	4	2	1.1	0.55	0.07	<a href="#">6-Sep</a>
PATIENT_4	<a href="#">chr1:11027601-11038497</a>	8	2	1.12	0.56	0.01	--
PATIENT_4	<a href="#">chr2:20510877-20511254</a>	3	2	1.13	0.56	0	--
PATIENT_4	<a href="#">chr3:47798169-47862990</a>	12	2	1.12	0.56	0.06	--
PATIENT_4	<a href="#">chr10:73662808-73904937</a>	16	2	1.12	0.56	0.24	--
PATIENT_4	<a href="#">chr12:48206278-48239825</a>	25	2	1.12	0.56	0.03	--
PATIENT_4	<a href="#">chr12:110566540-110764923</a>	49	2	1.12	0.56	0.2	<a href="#">ALDH2</a>
PATIENT_4	<a href="#">chr13:20374842-20613088</a>	22	2	1.12	0.56	0.24	<a href="#">LATS2</a>
PATIENT_4	<a href="#">chr14:49389191-49430535</a>	4	2	1.11	0.56	0.04	--
PATIENT_4	<a href="#">chr14:64077346-64078768</a>	7	2	1.13	0.56	0	--
PATIENT_4	<a href="#">chr14:101841042-102034250</a>	43	2	1.12	0.56	0.19	<a href="#">RAGE</a>
PATIENT_4	<a href="#">chr14:102460042-102480152</a>	16	2	1.11	0.56	0.02	<a href="#">CDC42BPB</a>
PATIENT_4	<a href="#">chr14:103039084-103070773</a>	13	2	1.12	0.56	0.03	<a href="#">MARK3</a>
PATIENT_4	<a href="#">chr16:79692300-79811313</a>	48	2	1.11	0.56	0.12	--
PATIENT_4	<a href="#">chr17:37372439-37374202</a>	5	2	1.12	0.56	0	--
PATIENT_4	<a href="#">chr19:6092579-11569431</a>	2085	2	1.11	0.56	5.48	CD70;DNMT1;INSR;MAP2K7;MLLT1; SMARCA4;TYK2
PATIENT_4	<a href="#">chr19:45009316-45178986</a>	82	2	1.13	0.56	0.17	<a href="#">DYRK1B</a>
PATIENT_4	<a href="#">chr19:48611922-48998340</a>	131	2	1.12	0.56	0.39	--
PATIENT_4	<a href="#">chr3:47137256-47626680</a>	147	2	1.15	0.57	0.49	<a href="#">SETD2</a>
PATIENT_4	<a href="#">chr7:56113321-56122884</a>	14	2	1.15	0.57	0.01	<a href="#">PHKG1</a>
PATIENT_4	<a href="#">chr9:19039752-19040427</a>	4	2	1.15	0.57	0	--
PATIENT_4	<a href="#">chr10:11837509-12003293</a>	8	2	1.14	0.57	0.17	--
PATIENT_4	<a href="#">chr10:43021466-43372718</a>	17	2	1.15	0.57	0.35	--
PATIENT_4	<a href="#">chr10:89110384-89114865</a>	3	2	1.14	0.57	0	--
PATIENT_4	<a href="#">chr11:76978766-76979256</a>	4	2	1.14	0.57	0	--
PATIENT_4	<a href="#">chr11:117981468-118039302</a>	46	2	1.14	0.57	0.06	--
PATIENT_4	<a href="#">chr12:111056988-111117159</a>	37	2	1.14	0.57	0.06	--
PATIENT_4	<a href="#">chr14:30667844-30673852</a>	7	2	1.15	0.57	0.01	--
PATIENT_4	<a href="#">chr14:103234980-103285950</a>	29	2	1.15	0.57	0.05	--
PATIENT_4	<a href="#">chr17:16061376-16306368</a>	44	2	1.13	0.57	0.24	--

PATIENT_4	<a href="#">chr17:34624597-34626894</a>	5	2	1.14	0.57	0	--
PATIENT_4	<a href="#">chr19:44640174-44715208</a>	59	2	1.13	0.57	0.08	--
PATIENT_4	<a href="#">chr19:59077643-60431476</a>	577	2	1.15	0.57	1.35	PRKCG;TFPT
PATIENT_4	<a href="#">chr1:27592938-27608830</a>	8	2	1.15	0.58	0.02	--
PATIENT_4	<a href="#">chr3:48476252-50393474</a>	1095	2	1.16	0.58	1.92	CAMKV;MST1R
PATIENT_4	<a href="#">chr4:39654528-39780998</a>	7	2	1.15	0.58	0.13	--
PATIENT_4	<a href="#">chr10:7658528-7662017</a>	6	2	1.15	0.58	0	--
PATIENT_4	<a href="#">chr11:65151520-65592748</a>	253	2	1.16	0.58	0.44	--
PATIENT_4	<a href="#">chr11:118162091-118390960</a>	53	2	1.15	0.58	0.23	--
PATIENT_4	<a href="#">chr12:47396616-48029750</a>	309	2	1.17	0.58	0.63	--
PATIENT_4	<a href="#">chr12:52162147-52185254</a>	25	2	1.16	0.58	0.02	<a href="#">MAP3K12</a>
PATIENT_4	<a href="#">chr12:118912286-119502043</a>	160	2	1.16	0.58	0.59	--
PATIENT_4	<a href="#">chr12:122637330-122737431</a>	46	2	1.16	0.58	0.1	--
PATIENT_4	<a href="#">chr14:21041260-21108560</a>	27	2	1.15	0.58	0.07	--
PATIENT_4	<a href="#">chr17:75695980-75697150</a>	6	2	1.16	0.58	0	--
PATIENT_4	<a href="#">chr19:47047540-47790771</a>	296	2	1.15	0.58	0.74	CD79A;CIC;GSK3A
PATIENT_4	<a href="#">chr20:2569891-3251301</a>	212	2	1.16	0.58	0.68	--
PATIENT_4	<a href="#">chr1:23993324-23996857</a>	12	2	1.18	0.59	0	--
PATIENT_4	<a href="#">chr2:25048228-25322554</a>	40	2	1.18	0.59	0.27	<a href="#">DNMT3A</a>
PATIENT_4	<a href="#">chr2:45025294-45089706</a>	5	2	1.18	0.59	0.06	--
PATIENT_4	<a href="#">chr7:128588772-128639345</a>	19	2	1.18	0.59	0.05	<a href="#">SMO</a>
PATIENT_4	<a href="#">chr7:151763714-151774730</a>	10	2	1.17	0.59	0.01	<a href="#">MLL3</a>
PATIENT_4	<a href="#">chr8:37805948-38124942</a>	84	2	1.17	0.59	0.32	--
PATIENT_4	<a href="#">chr9:130508867-130748921</a>	111	2	1.19	0.59	0.24	<a href="#">PKN3</a>
PATIENT_4	<a href="#">chr11:62305982-62412224</a>	71	2	1.18	0.59	0.11	--
PATIENT_4	<a href="#">chr12:51491884-52134884</a>	303	2	1.18	0.59	0.64	<a href="#">AMHR2</a>
PATIENT_4	<a href="#">chr14:104488938-105308726</a>	207	2	1.17	0.59	0.82	--
PATIENT_4	<a href="#">chr16:31120506-31143456</a>	12	2	1.19	0.59	0.02	--
PATIENT_4	<a href="#">chr16:66774694-69290124</a>	484	2	1.18	0.59	2.52	<a href="#">CDH1</a>
PATIENT_4	<a href="#">chr19:37780993-39611238</a>	239	2	1.19	0.59	1.83	--
PATIENT_4	<a href="#">chrX:118870830-118889938</a>	8	2	1.18	0.59	0.02	--
PATIENT_4	<a href="#">chr1:46419385-46647406</a>	86	2	1.19	0.6	0.23	--
PATIENT_4	<a href="#">chr3:47005202-47025751</a>	61	2	1.21	0.6	0.02	--

PATIENT_4	<a href="#">chr4:505031-1008992</a>	158	2	1.2	0.6	0.5	<a href="#">GAK</a>
PATIENT_4	<a href="#">chr4:8633704-8672206</a>	17	2	1.21	0.6	0.04	--
PATIENT_4	<a href="#">chr4:25273280-25368296</a>	17	2	1.19	0.6	0.1	--
PATIENT_4	<a href="#">chr7:72589582-73653365</a>	217	2	1.2	0.6	1.06	ELN;LIMK1
PATIENT_4	<a href="#">chr10:103567663-103593269</a>	12	2	1.2	0.6	0.03	--
PATIENT_4	<a href="#">chr10:103860354-104669545</a>	261	2	1.2	0.6	0.81	NFKB2;SUFU
PATIENT_4	<a href="#">chr10:115793972-115794439</a>	3	2	1.2	0.6	0	--
PATIENT_4	<a href="#">chr10:126676682-126705999</a>	12	2	1.2	0.6	0.03	--
PATIENT_4	<a href="#">chr11:66801342-66982678</a>	136	2	1.2	0.6	0.18	ADRBK1;RPS6KB2
PATIENT_4	<a href="#">chr11:116539754-116614801</a>	51	2	1.21	0.6	0.08	PAFAH1B2;PCSK7
PATIENT_4	<a href="#">chr11:118394192-118582371</a>	163	2	1.2	0.6	0.19	<a href="#">CBL</a>
PATIENT_4	<a href="#">chr12:7696674-8126188</a>	66	2	1.19	0.6	0.43	--
PATIENT_4	<a href="#">chr12:111980589-112393592</a>	142	2	1.2	0.6	0.41	--
PATIENT_4	<a href="#">chr12:130889172-132098042</a>	339	2	1.2	0.6	1.21	<a href="#">ULK1</a>
PATIENT_4	<a href="#">chr14:72781152-72820698</a>	32	2	1.2	0.6	0.04	--
PATIENT_4	<a href="#">chr14:72896572-73035572</a>	23	2	1.21	0.6	0.14	--
PATIENT_4	<a href="#">chr16:65768282-65894650</a>	150	2	1.21	0.6	0.13	--
PATIENT_4	<a href="#">chr16:72896813-74043158</a>	160	2	1.2	0.6	1.15	<a href="#">MLKL</a>
PATIENT_4	<a href="#">chr16:85922397-88559823</a>	619	2	1.2	0.6	2.64	CBFA2T3;CDK10;FANCA
PATIENT_4	<a href="#">chr17:6843038-8237429</a>	966	2	1.2	0.6	1.39	AURKB;GUCY2D;PER1;TP53
PATIENT_4	<a href="#">chr17:19522726-19588932</a>	27	2	1.19	0.6	0.07	--
PATIENT_4	<a href="#">chr17:40180338-40238586</a>	38	2	1.21	0.6	0.06	--
PATIENT_4	<a href="#">chr20:3597630-3794475</a>	128	2	1.2	0.6	0.2	--
PATIENT_4	<a href="#">chr1:6450207-6453696</a>	13	2	1.23	0.61	0	--
PATIENT_4	<a href="#">chr10:121419470-121426778</a>	10	2	1.22	0.61	0.01	--
PATIENT_4	<a href="#">chr10:123832210-123837350</a>	30	2	1.22	0.61	0.01	--
PATIENT_4	<a href="#">chr11:63032644-64968510</a>	800	2	1.21	0.61	1.94	CDC42BPG;MAP4K2;MARK2;MEN1;RPS6KA4
PATIENT_4	<a href="#">chr11:116657924-116714546</a>	16	2	1.23	0.61	0.06	--
PATIENT_4	<a href="#">chr11:118674362-118722395</a>	42	2	1.22	0.61	0.05	<a href="#">CBL</a>
PATIENT_4	<a href="#">chr11:129573002-129584838</a>	9	2	1.21	0.61	0.01	--
PATIENT_4	<a href="#">chr12:19413938-19506808</a>	4	2	1.21	0.61	0.09	--
PATIENT_4	<a href="#">chr12:54480636-55728303</a>	633	2	1.23	0.61	1.25	CDK2;ERBB3;NACA
PATIENT_4	<a href="#">chr12:119572846-119589054</a>	7	2	1.22	0.61	0.02	--
PATIENT_4	<a href="#">chr12:121804247-122534732</a>	194	2	1.22	0.61	0.73	--
PATIENT_4	<a href="#">chr13:79808984-79809757</a>	5	2	1.21	0.61	0	--

PATIENT_4	<a href="#">chr14:22309278-22375916</a>	23	2	1.22	0.61	0.07	--
PATIENT_4	<a href="#">chr14:63135258-63264202</a>	13	2	1.23	0.61	0.13	--
PATIENT_4	<a href="#">chr14:72474494-72608148</a>	29	2	1.22	0.61	0.13	--
PATIENT_4	<a href="#">chr16:24791000-24850203</a>	17	2	1.22	0.61	0.06	--
PATIENT_4	<a href="#">chr16:65438538-65760684</a>	124	2	1.22	0.61	0.32	<a href="#">CBFB</a>
PATIENT_4	<a href="#">chr17:18796295-19495570</a>	104	2	1.22	0.61	0.7	<a href="#">MAPK7</a>
PATIENT_4	<a href="#">chr17:26725224-27298775</a>	44	2	1.23	0.61	0.57	NF1;SUZ12
PATIENT_4	<a href="#">chr22:30330885-30439665</a>	33	2	1.22	0.61	0.11	--
PATIENT_4	<a href="#">chr1:28049314-28082012</a>	11	2	1.24	0.62	0.03	--
PATIENT_4	<a href="#">chr1:153557240-153563342</a>	19	2	1.25	0.62	0.01	--
PATIENT_4	<a href="#">chr2:26385466-26422577</a>	23	2	1.25	0.62	0.04	--
PATIENT_4	<a href="#">chr4:2222684-2847484</a>	71	2	1.24	0.62	0.62	--
PATIENT_4	<a href="#">chr5:137617419-137638002</a>	7	2	1.24	0.62	0.02	--
PATIENT_4	<a href="#">chr5:176382432-176494708</a>	26	2	1.24	0.62	0.11	FGFR4;NSD1
PATIENT_4	<a href="#">chr11:56950127-57326105</a>	97	2	1.24	0.62	0.38	--
PATIENT_4	<a href="#">chr14:22382840-22414156</a>	12	2	1.24	0.62	0.03	--
PATIENT_4	<a href="#">chr14:99662822-99775848</a>	21	2	1.25	0.62	0.11	--
PATIENT_4	<a href="#">chr14:99828596-99878568</a>	16	2	1.24	0.62	0.05	--
PATIENT_4	<a href="#">chr14:101521858-101574861</a>	59	2	1.24	0.62	0.05	--
PATIENT_4	<a href="#">chr17:1906363-2531806</a>	124	2	1.24	0.62	0.63	--
PATIENT_4	<a href="#">chr17:27619040-27701426</a>	20	2	1.25	0.62	0.08	--
PATIENT_4	<a href="#">chr21:9884506-9884914</a>	4	2	1.24	0.62	0	--
PATIENT_4	<a href="#">chr3:47873955-48456981</a>	140	2	1.25	0.63	0.58	--
PATIENT_4	<a href="#">chr4:3288299-3289474</a>	7	2	1.26	0.63	0	--
PATIENT_4	<a href="#">chr6:18230052-18230606</a>	4	2	1.27	0.63	0	--
PATIENT_4	<a href="#">chr10:71684882-72138474</a>	51	2	1.26	0.63	0.45	<a href="#">PRF1</a>
PATIENT_4	<a href="#">chr11:62500881-62538832</a>	21	2	1.25	0.63	0.04	--
PATIENT_4	<a href="#">chr12:49034583-49185232</a>	30	2	1.25	0.63	0.15	--
PATIENT_4	<a href="#">chr12:49668430-50105066</a>	95	2	1.26	0.63	0.44	--
PATIENT_4	<a href="#">chr12:115456880-115758420</a>	20	2	1.26	0.63	0.3	--
PATIENT_4	<a href="#">chr12:116111478-116389378</a>	35	2	1.25	0.63	0.28	--
PATIENT_4	<a href="#">chr13:19244390-19466052</a>	21	2	1.27	0.63	0.22	--
PATIENT_4	<a href="#">chr14:101584090-101786979</a>	38	2	1.27	0.63	0.2	<a href="#">RAGE</a>
PATIENT_4	<a href="#">chr16:56877340-57112407</a>	33	2	1.25	0.63	0.24	--

PATIENT_4	<a href="#">chr17:131593-564651</a>	33	2	1.27	0.63	0.43	--
PATIENT_4	<a href="#">chr17:24000248-25054138</a>	346	2	1.26	0.63	1.05	NEK8;TAOK1
PATIENT_4	<a href="#">chr17:39990719-40090067</a>	10	2	1.25	0.63	0.1	--
PATIENT_4	<a href="#">chr19:13737840-14061026</a>	159	2	1.26	0.63	0.32	--
PATIENT_4	<a href="#">chr19:50347895-50348760</a>	7	2	1.26	0.63	0	--
PATIENT_4	<a href="#">chr19:60795726-61427998</a>	196	2	1.25	0.63	0.63	--
PATIENT_4	<a href="#">chrX:54489317-54513821</a>	20	2	1.26	0.63	0.02	--
PATIENT_4	<a href="#">chr1:92714254-92721569</a>	6	2	1.28	0.64	0.01	--
PATIENT_4	<a href="#">chr1:152810326-152814938</a>	5	2	1.29	0.64	0	--
PATIENT_4	<a href="#">chr3:9491186-10392212</a>	338	2	1.28	0.64	0.9	CAMK1;FANCD2;IRAK2;VHL
PATIENT_4	<a href="#">chr3:197409642-197450030</a>	17	2	1.28	0.64	0.04	--
PATIENT_4	<a href="#">chr3:197529350-197538734</a>	5	2	1.29	0.64	0.01	--
PATIENT_4	<a href="#">chr4:1196750-2053204</a>	165	2	1.28	0.64	0.86	FGFR3;WHSC1
PATIENT_4	<a href="#">chr7:72049392-72494594</a>	60	2	1.28	0.64	0.45	--
PATIENT_4	<a href="#">chr9:33375119-33907902</a>	59	2	1.28	0.64	0.53	--
PATIENT_4	<a href="#">chr10:74928495-75345086</a>	169	2	1.28	0.64	0.42	<a href="#">CAMK2G</a>
PATIENT_4	<a href="#">chr10:104995884-105193000</a>	70	2	1.29	0.64	0.2	--
PATIENT_4	<a href="#">chr11:60424926-62300472</a>	667	2	1.27	0.64	1.88	--
PATIENT_4	<a href="#">chr11:113308934-113532319</a>	22	2	1.28	0.64	0.22	--
PATIENT_4	<a href="#">chr12:2776630-3259856</a>	79	2	1.28	0.64	0.48	--
PATIENT_4	<a href="#">chr13:40602683-40666311</a>	21	2	1.28	0.64	0.06	--
PATIENT_4	<a href="#">chr14:73130268-73839349</a>	159	2	1.27	0.64	0.71	--
PATIENT_4	<a href="#">chr16:66202775-66229188</a>	11	2	1.29	0.64	0.03	--
PATIENT_4	<a href="#">chr17:16783680-18338326</a>	402	2	1.28	0.64	1.55	<a href="#">FLCN</a>
PATIENT_4	<a href="#">chr17:25910896-26446473</a>	76	2	1.28	0.64	0.54	<a href="#">NF1</a>
PATIENT_4	<a href="#">chr17:34935860-35038984</a>	11	2	1.29	0.64	0.1	--
PATIENT_4	<a href="#">chr18:22381084-22381844</a>	4	2	1.29	0.64	0	--
PATIENT_4	<a href="#">chr19:53344868-53481901</a>	25	2	1.29	0.64	0.14	--
PATIENT_4	<a href="#">chr19:61824643-63702022</a>	599	2	1.29	0.64	1.88	<a href="#">AURKC</a>
PATIENT_4	<a href="#">chr21:36525082-36540600</a>	12	2	1.28	0.64	0.02	--
PATIENT_4	<a href="#">chr22:16407996-16450758</a>	16	2	1.28	0.64	0.04	--
PATIENT_4	<a href="#">chrX:46318456-46319290</a>	4	2	1.29	0.64	0	--
PATIENT_4	<a href="#">chr1:67628344-67634333</a>	4	2	1.3	0.65	0.01	--
PATIENT_4	<a href="#">chr2:24061064-24092600</a>	5	2	1.3	0.65	0.03	--

PATIENT_4	<a href="#">chr2:53934372-53935368</a>	7	2	1.29	0.65	0	--
PATIENT_4	<a href="#">chr3:53187528-53301885</a>	38	2	1.3	0.65	0.11	<a href="#">PRKCD</a>
PATIENT_4	<a href="#">chr4:2870856-2935622</a>	41	2	1.31	0.65	0.06	<a href="#">GRK4</a>
PATIENT_4	<a href="#">chr4:39044224-39115862</a>	9	2	1.31	0.65	0.07	--
PATIENT_4	<a href="#">chr7:6406322-6628353</a>	73	2	1.3	0.65	0.22	--
PATIENT_4	<a href="#">chr7:99866174-102099237</a>	666	2	1.29	0.65	2.23	<a href="#">EPHB4</a>
PATIENT_4	<a href="#">chr7:127771024-128375529</a>	196	2	1.31	0.65	0.6	--
PATIENT_4	<a href="#">chr10:88673154-88803118</a>	32	2	1.29	0.65	0.13	<a href="#">BMPR1A</a>
PATIENT_4	<a href="#">chr12:116777660-116956439</a>	15	2	1.3	0.65	0.18	--
PATIENT_4	<a href="#">chr12:121282767-121676712</a>	138	2	1.31	0.65	0.39	--
PATIENT_4	<a href="#">chr13:18221912-18653904</a>	9	2	1.31	0.65	0.43	--
PATIENT_4	<a href="#">chr14:88015230-88016376</a>	7	2	1.31	0.65	0	--
PATIENT_4	<a href="#">chr14:90696430-90875457</a>	49	2	1.3	0.65	0.18	--
PATIENT_4	<a href="#">chr14:103628772-104486182</a>	215	2	1.31	0.65	0.86	<a href="#">AKT1</a>
PATIENT_4	<a href="#">chr17:3344435-3378110</a>	10	2	1.29	0.65	0.03	--
PATIENT_4	<a href="#">chr18:7040814-7222032</a>	8	2	1.3	0.65	0.18	--
PATIENT_4	<a href="#">chr19:34857214-35005266</a>	16	2	1.3	0.65	0.15	--
PATIENT_4	<a href="#">chr19:39673166-39777276</a>	10	2	1.29	0.65	0.1	--
PATIENT_4	<a href="#">chr20:5969776-5981424</a>	13	2	1.3	0.65	0.01	--
PATIENT_4	<a href="#">chr1:28349246-29186954</a>	100	2	1.32	0.66	0.84	--
PATIENT_4	<a href="#">chr1:31304802-31433495</a>	7	2	1.32	0.66	0.13	--
PATIENT_4	<a href="#">chr1:46260267-46282024</a>	22	2	1.33	0.66	0.02	<a href="#">MAST2</a>
PATIENT_4	<a href="#">chr1:63561438-63562190</a>	5	2	1.32	0.66	0	--
PATIENT_4	<a href="#">chr1:200224720-200364224</a>	28	2	1.32	0.66	0.14	--
PATIENT_4	<a href="#">chr2:109729931-109730352</a>	4	2	1.32	0.66	0	--
PATIENT_4	<a href="#">chr5:78568426-78569218</a>	5	2	1.33	0.66	0	--
PATIENT_4	<a href="#">chr8:27201137-27224502</a>	9	2	1.33	0.66	0.02	--
PATIENT_4	<a href="#">chr8:33366155-33574460</a>	37	2	1.32	0.66	0.21	--
PATIENT_4	<a href="#">chr9:700920-906826</a>	30	2	1.31	0.66	0.21	--
PATIENT_4	<a href="#">chr9:33916632-34078415</a>	31	2	1.32	0.66	0.16	--
PATIENT_4	<a href="#">chr9:37493116-37531372</a>	16	2	1.33	0.66	0.04	--
PATIENT_4	<a href="#">chr10:69595518-71232222</a>	299	2	1.33	0.66	1.64	--
PATIENT_4	<a href="#">chr11:107168626-107385264</a>	12	2	1.32	0.66	0.22	--
PATIENT_4	<a href="#">chr12:99075116-99118788</a>	5	2	1.33	0.66	0.04	--
PATIENT_4	<a href="#">chr13:99415668-99539424</a>	11	2	1.32	0.66	0.12	--

PATIENT_4	<a href="#">chr14:54599182-54674707</a>	8	2	1.33	0.66	0.08	--
PATIENT_4	<a href="#">chr14:73944322-73946183</a>	5	2	1.32	0.66	0	--
PATIENT_4	<a href="#">chr16:55974394-56720470</a>	220	2	1.31	0.66	0.75	--
PATIENT_4	<a href="#">chr17:34811151-34881509</a>	43	2	1.31	0.66	0.07	--
PATIENT_4	<a href="#">chr19:51067493-51534662</a>	76	2	1.32	0.66	0.47	--
PATIENT_4	<a href="#">chr1:19842406-19893558</a>	11	2	1.33	0.67	0.05	--
PATIENT_4	<a href="#">chr1:21981973-22206516</a>	124	2	1.35	0.67	0.22	--
PATIENT_4	<a href="#">chr2:26252776-26271528</a>	15	2	1.35	0.67	0.02	--
PATIENT_4	<a href="#">chr2:26525118-27451964</a>	350	2	1.34	0.67	0.93	--
PATIENT_4	<a href="#">chr5:177415438-17751338</a>	26	2	1.35	0.67	0.1	--
PATIENT_4	<a href="#">chr7:64975870-65184830</a>	19	2	1.34	0.67	0.21	--
PATIENT_4	<a href="#">chr7:73807762-75981236</a>	195	2	1.34	0.67	2.17	<a href="#">HIP1</a>
PATIENT_4	<a href="#">chr10:88249949-88475919</a>	34	2	1.34	0.67	0.23	--
PATIENT_4	<a href="#">chr10:99203325-99521340</a>	94	2	1.34	0.67	0.32	--
PATIENT_4	<a href="#">chr10:101705072-101901991</a>	22	2	1.34	0.67	0.2	--
PATIENT_4	<a href="#">chr11:122353648-122953394</a>	26	2	1.34	0.67	0.6	--
PATIENT_4	<a href="#">chr12:5900650-7234426</a>	577	2	1.34	0.67	1.33	<a href="#">ZNF384</a>
PATIENT_4	<a href="#">chr12:45915242-45916362</a>	5	2	1.34	0.67	0	--
PATIENT_4	<a href="#">chr13:31783563-31784014</a>	3	2	1.34	0.67	0	--
PATIENT_4	<a href="#">chr14:103096009-103223218</a>	29	2	1.35	0.67	0.13	--
PATIENT_4	<a href="#">chr15:40627651-40628412</a>	3	2	1.35	0.67	0	--
PATIENT_4	<a href="#">chr16:28130184-31101424</a>	948	2	1.33	0.67	2.97	BCKDK;FUS;MAPK3;PHKG2;SBK1; <a href="#">TAOK2</a>
PATIENT_4	<a href="#">chr17:2807822-3283878</a>	75	2	1.34	0.67	0.48	--
PATIENT_4	<a href="#">chr20:186429-376611</a>	63	2	1.35	0.67	0.19	<a href="#">TRIB3</a>
PATIENT_4	<a href="#">chr20:577464-896744</a>	31	2	1.35	0.67	0.32	--
PATIENT_4	<a href="#">chr22:22416633-22454512</a>	23	2	1.34	0.67	0.04	--
PATIENT_4	<a href="#">chrX:128974990-12897770</a>	15	2	1.35	0.67	0	--
PATIENT_4	<a href="#">chr1:2508490-2550739</a>	30	2	1.36	0.68	0.04	--
PATIENT_4	<a href="#">chr1:23392347-23509802</a>	7	2	1.37	0.68	0.12	--
PATIENT_4	<a href="#">chr2:38666415-38909026</a>	38	2	1.35	0.68	0.24	--
PATIENT_4	<a href="#">chr2:42524664-43360468</a>	44	2	1.36	0.68	0.84	--
PATIENT_4	<a href="#">chr2:171281256-171282078</a>	3	2	1.35	0.68	0	--
PATIENT_4	<a href="#">chr2:208340052-208401390</a>	8	2	1.36	0.68	0.06	--

PATIENT_4	<a href="#">chr3:51367415-51424916</a>	31	2	1.36	0.68	0.06	--
PATIENT_4	<a href="#">chr3:51432368-52267629</a>	226	2	1.37	0.68	0.84	--
PATIENT_4	<a href="#">chr3:52299481-52418908</a>	113	2	1.36	0.68	0.12	<a href="#">BAP1</a>
PATIENT_4	<a href="#">chr5:139927358-139999556</a>	12	2	1.36	0.68	0.07	--
PATIENT_4	<a href="#">chr6:32171730-32173690</a>	9	2	1.36	0.68	0	--
PATIENT_4	<a href="#">chr8:8213181-8787778</a>	38	2	1.36	0.68	0.57	--
PATIENT_4	<a href="#">chr8:28242650-28274410</a>	14	2	1.37	0.68	0.03	--
PATIENT_4	<a href="#">chr8:28983940-28985187</a>	3	2	1.36	0.68	0	--
PATIENT_4	<a href="#">chr9:37412776-37476736</a>	21	2	1.36	0.68	0.06	--
PATIENT_4	<a href="#">chr9:133062499-133063984</a>	8	2	1.35	0.68	0	<a href="#">NUP214</a>
PATIENT_4	<a href="#">chr10:21454927-21846478</a>	19	2	1.36	0.68	0.39	--
PATIENT_4	<a href="#">chr10:22088152-22088446</a>	3	2	1.36	0.68	0	--
PATIENT_4	<a href="#">chr10:99130590-99193016</a>	24	2	1.37	0.68	0.06	--
PATIENT_4	<a href="#">chr10:105208446-105474050</a>	31	2	1.35	0.68	0.27	--
PATIENT_4	<a href="#">chr11:116166184-116235349</a>	22	2	1.36	0.68	0.07	--
PATIENT_4	<a href="#">chr12:342441-1062764</a>	112	2	1.35	0.68	0.72	KDM5A;WNK1
PATIENT_4	<a href="#">chr12:31331903-32421780</a>	86	2	1.37	0.68	1.09	--
PATIENT_4	<a href="#">chr12:48240006-49031448</a>	234	2	1.36	0.68	0.79	--
PATIENT_4	<a href="#">chr12:54231695-54437576</a>	63	2	1.35	0.68	0.21	--
PATIENT_4	<a href="#">chr12:55758716-56625690</a>	507	2	1.36	0.68	0.87	CDK4;DDIT3
PATIENT_4	<a href="#">chr12:113594235-113605224</a>	11	2	1.37	0.68	0.01	--
PATIENT_4	<a href="#">chr12:117073264-117298948</a>	21	2	1.36	0.68	0.23	<a href="#">TAOK3</a>
PATIENT_4	<a href="#">chr14:60816800-60858712</a>	4	2	1.36	0.68	0.04	<a href="#">PRKCH</a>
PATIENT_4	<a href="#">chr16:45302118-45675088</a>	40	2	1.36	0.68	0.37	--
PATIENT_4	<a href="#">chr16:66256477-66259078</a>	7	2	1.37	0.68	0	--
PATIENT_4	<a href="#">chr17:4935714-6433910</a>	208	2	1.36	0.68	1.5	<a href="#">USP6</a>
PATIENT_4	<a href="#">chr17:23627824-23994364</a>	207	2	1.36	0.68	0.37	--
PATIENT_4	<a href="#">chr18:27776630-27926774</a>	8	2	1.35	0.68	0.15	--
PATIENT_4	<a href="#">chr18:53178458-53255168</a>	7	2	1.35	0.68	0.08	--
PATIENT_4	<a href="#">chr18:58796480-59136752</a>	11	2	1.35	0.68	0.34	<a href="#">BCL2</a>
PATIENT_4	<a href="#">chr19:41730404-42338972</a>	104	2	1.35	0.68	0.61	--
PATIENT_4	<a href="#">chr1:51385855-51560374</a>	22	2	1.38	0.69	0.17	--
PATIENT_4	<a href="#">chr1:62352395-62519810</a>	39	2	1.37	0.69	0.17	--

PATIENT_4	<a href="#">chr1:113019121-113536716</a>	70	2	1.38	0.69	0.52	--
PATIENT_4	<a href="#">chr2:27456590-27740848</a>	190	2	1.38	0.69	0.28	<a href="#">NRBP1</a>
PATIENT_4	<a href="#">chr2:32591605-32594314</a>	4	2	1.38	0.69	0	--
PATIENT_4	<a href="#">chr2:218930174-219005070</a>	44	2	1.39	0.69	0.07	--
PATIENT_4	<a href="#">chr2:223229003-22344790</a>	2	2	1.38	0.69	0.02	--
PATIENT_4	<a href="#">chr3:11275810-11325490</a>	10	2	1.39	0.69	0.05	--
PATIENT_4	<a href="#">chr3:12586631-13835864</a>	160	2	1.38	0.69	1.25	<a href="#">RAF1</a>
PATIENT_4	<a href="#">chr3:32586872-32790022</a>	21	2	1.38	0.69	0.2	--
PATIENT_4	<a href="#">chr4:189161305-189255254</a>	6	2	1.38	0.69	0.09	--
PATIENT_4	<a href="#">chr9:109287926-109291254</a>	13	2	1.38	0.69	0	--
PATIENT_4	<a href="#">chr9:125814528-125834648</a>	7	2	1.39	0.69	0.02	--
PATIENT_4	<a href="#">chr9:127009746-127043160</a>	18	2	1.38	0.69	0.03	--
PATIENT_4	<a href="#">chr10:15153835-15366094</a>	40	2	1.38	0.69	0.21	--
PATIENT_4	<a href="#">chr10:35895092-35970131</a>	16	2	1.37	0.69	0.08	--
PATIENT_4	<a href="#">chr11:71424604-72238511</a>	186	2	1.38	0.69	0.81	<a href="#">NUMA1</a>
PATIENT_4	<a href="#">chr11:86340758-86426796</a>	6	2	1.38	0.69	0.09	--
PATIENT_4	<a href="#">chr12:110787457-111052728</a>	52	2	1.39	0.69	0.27	--
PATIENT_4	<a href="#">chr13:94656902-95010463</a>	11	2	1.38	0.69	0.35	--
PATIENT_4	<a href="#">chr15:38798333-39059808</a>	105	2	1.39	0.69	0.26	--
PATIENT_4	<a href="#">chr15:41953432-41953932</a>	4	2	1.38	0.69	0	--
PATIENT_4	<a href="#">chr18:3267922-3719242</a>	19	2	1.39	0.69	0.45	--
PATIENT_4	<a href="#">chr18:54565676-54752741</a>	16	2	1.37	0.69	0.19	<a href="#">MALT1</a>
PATIENT_4	<a href="#">chr19:56214140-58687151</a>	674	2	1.38	0.69	2.47	<a href="#">PPP2R1A</a>
PATIENT_4	<a href="#">chrX:48202312-49030476</a>	388	2	1.39	0.69	0.83	GATA1;PIM2;TFE3;WAS
PATIENT_4	<a href="#">chrX:70753030-70755012</a>	7	2	1.39	0.69	0	--
PATIENT_4	<a href="#">chr3:52444719-52842422</a>	291	2	1.4	0.7	0.4	NEK4;PBRM1
PATIENT_4	<a href="#">chr4:189297900-189305469</a>	9	2	1.4	0.7	0.01	--
PATIENT_4	<a href="#">chr7:4247997-5507247</a>	155	2	1.4	0.7	1.26	--
PATIENT_4	<a href="#">chr7:130841256-130846667</a>	9	2	1.4	0.7	0.01	--
PATIENT_4	<a href="#">chr9:6496103-6839607</a>	31	2	1.39	0.7	0.34	--
PATIENT_4	<a href="#">chr11:93678548-93773790</a>	10	2	1.39	0.7	0.1	--
PATIENT_4	<a href="#">chr12:107486763-110220760</a>	487	2	1.4	0.7	2.73	--
PATIENT_4	<a href="#">chr13:19614209-19961559</a>	19	2	1.4	0.7	0.35	--

PATIENT_4	<a href="#"><u>chr15:39167122-39660734</u></a>	149	2	1.39	0.7	0.49	LTK;TYRO3
PATIENT_4	<a href="#"><u>chr15:88136474-88610012</u></a>	95	2	1.39	0.7	0.47	<a href="#"><u>IDH2</u></a>
PATIENT_4	<a href="#"><u>chr16:15637202-16204856</u></a>	123	2	1.4	0.7	0.57	<a href="#"><u>MYH11</u></a>
PATIENT_4	<a href="#"><u>chr16:57307524-57325572</u></a>	8	2	1.4	0.7	0.02	--
PATIENT_4	<a href="#"><u>chr16:74121765-74247982</u></a>	43	2	1.4	0.7	0.13	--
PATIENT_4	<a href="#"><u>chr17:3671339-3712294</u></a>	10	2	1.39	0.7	0.04	<a href="#"><u>CAMKK1</u></a>
PATIENT_4	<a href="#"><u>chr17:3801368-4157106</u></a>	98	2	1.4	0.7	0.36	--
PATIENT_4	<a href="#"><u>chr22:39576795-40406257</u></a>	212	2	1.4	0.7	0.83	<a href="#"><u>EP300</u></a>

**Table S13: Structural Variation by Patient**

Patient	Gene1	Gene2	Genome position 1	Genome position 2	Type	Size	Score	Supporting Reads
Patient 1	LOC387647	LOC387647	chr10:29752135	chr10:29752726	DEL	619	99	7
Patient 1	intergenic	intergenic	chr10:38856454	chr10:38857601	DEL	1253	99	5
Patient 1	intergenic	intergenic	chr10:41705339	chr10:41715989	DEL	10451	99	4
Patient 1	GALNTL4	GALNTL4	chr11:11336179	chr11:11337669	DEL	1437	99	6
Patient 1	intergenic	intergenic	chr11:48557417	chr11:48560938	DEL	3422	85	3
Patient 1	intergenic	intergenic	chr11:65775225	chr11:65776393	INV	639	99	6
Patient 1	intergenic	intergenic	chr11:70989034	chr11:71288824	ITX	299089	99	4
Patient 1	BC048427	BC048427	chr11:73702508	chr11:73705149	DEL	2495	99	4
Patient 1	intergenic	intergenic	chr11:103772916	chr11:103778559	DEL	5530	83	3
Patient 1	intergenic	intergenic	chr12:6408470	chr12:6409018	DEL	413	86	3
Patient 1	intergenic	intergenic	chr12:30369433	chr12:30372291	DEL	2727	87	3
Patient 1	intergenic	intergenic	chr12:68881091	chr12:68883990	DEL	2754	82	3
Patient 1	intergenic	intergenic	chr13:19723437	chr13:19726913	DEL	3335	89	3
Patient 1	ZDHHC20	intergenic	chr13:20914965	chr13:36751019	INV	15835609	90	3
Patient 1	intergenic	intergenic	chr13:83831240	chr13:84205136	DEL	373804	99	6
Patient 1	intergenic	intergenic	chr13:84276078	chr13:84278640	INV	1905	99	5
Patient 1	intergenic	intergenic	chr13:36711225	chr13:103743336	INV	67031604	99	3
Patient 1	intergenic	intergenic	chr14:28797777	chr14:28798640	DEL	784	81	3
Patient 1	intergenic	TRMT5	chr14:60164765	chr14:60512187	INV	347008	94	3
Patient 1	intergenic	intergenic	chr14:84366816	chr14:84371946	DEL	5079	99	4
Patient 1	intergenic	intergenic	chr15:19048227	chr15:21007100	ITX	1958179	99	3
Patient 1	KIAA1454,SC APER	KIAA1454,S CAPER	chr15:74671448	chr15:74684012	DEL	12375	95	3
Patient 1	intergenic	intergenic	chr15:75795518	chr15:75799859	DEL	4115	99	3
Patient 1	intergenic	intergenic	chr16:44944231	chr16:44957505	DEL	13392	99	4
Patient 1	SNTB2	intergenic	chr16:67843541	chr16:70105976	DEL	2262310	99	5
Patient 1	CALB2	intergenic	chr16:69954967	chr16:70835609	ITX	879792	99	7
Patient 1	intergenic	intergenic	chr16:84186557	chr16:84187983	INV	772	93	3
Patient 1	SPIRE2	SPIRE2	chr16:88423363	chr16:88425909	DEL	2383	92	3
Patient 1	NT5M	NT5M	chr17:17171070	chr17:17172066	DEL	879	87	3
Patient 1	PRPSAP2	PRPSAP2	chr17:18731829	chr17:18732968	DEL	1054	99	4
Patient 1	intergenic	intergenic	chr17:22287260	chr17:22289206	ITX	1217	99	4
Patient 1	ERN1	PRKCA	chr17:59529849	chr17:61893264	ITX	2362632	99	4
Patient 1	intergenic	ROCK1	chr18:97992	chr18:99692	ITX	427	99	5
Patient 1	CDH7,CDH19	CDH7,CDH19	chr18:62370650	chr18:62372293	DEL	1593	99	5
Patient 1	intergenic	intergenic	chr19:20593012	chr19:20675604	INV	82137	99	4
Patient 1	intergenic	intergenic	chr19:32424165	chr19:32428056	DEL	3821	99	6
Patient 1	intergenic	intergenic	chr19:32424165	chr19:32430235	DEL	6106	99	23
Patient 1	intergenic	intergenic	chr19:37778836	chr19:37779043	ITX	-438	90	3
Patient 1	AF086165	intergenic	chr19:57580610	chr19:57583192	DEL	2602	99	5
Patient 1	ZNF765	ZNF765	chr19:58605172	chr19:58606610	DEL	1370	99	5
Patient 1	SLC1A7	SLC1A7	chr1:53367708	chr1:53368188	DEL	477	82	3
Patient 1	intergenic	intergenic	chr1:56603702	chr1:56607558	DEL	3906	99	6
Patient 1	intergenic	intergenic	chr1:81177097	chr1:81183543	DEL	6206	99	3
Patient 1	intergenic	intergenic	chr1:87689526	chr1:87689834	ITX	-441	99	4
Patient 1	intergenic	intergenic	chr19:32424165	chr1:121185259	CTX	-452	99	1309
Patient 1	intergenic	intergenic	chr19:32425324	chr1:121185259	CTX	-452	99	89
Patient 1	intergenic	intergenic	chr19:32425797	chr1:121185259	CTX	-452	99	11
Patient 1	intergenic	intergenic	chr19:32428636	chr1:121185259	CTX	-452	99	10
Patient 1	intergenic	intergenic	chr19:32430529	chr1:121185259	CTX	-452	99	140
Patient 1	intergenic	intergenic	chr1:157134020	chr1:157136609	DEL	2446	88	3
Patient 1	intergenic	intergenic	chr1:173466982	chr1:173468557	INV	1122	99	4
Patient 1	intergenic	intergenic	chr20:16116998	chr20:16117130	ITX	-438	95	3
Patient 1	intergenic	intergenic	chr21:9727557	chr21:9729308	ITX	-414	99	8
Patient 1	intergenic	intergenic	chr21:13272246	chr21:13283910	DEL	11837	99	4
Patient 1	intergenic	intergenic	chr21:13281131	chr21:13282946	DEL	1611	99	4
Patient 1	intergenic	intergenic	chr21:26942378	chr21:26943518	INV	648	99	4
Patient 1	intergenic	DDTL	chr22:22604099	chr22:22641460	DEL	37194	99	4
Patient 1	intergenic	intergenic	chr22:35473118	chr22:35478118	DEL	4781	99	3

Patient 1	SNTG2	SNTG2	chr2:1337038	chr2:1337485	DEL	467	99	8
Patient 1	intergenic	intergenic	chr2:42199743	chr2:42200876	DEL	1057	82	3
Patient 1	intergenic	intergenic	chr2:48843842	chr2:48844696	DEL	660	99	4
Patient 1	intergenic	intergenic	chr2:70514724	chr2:70515956	DEL	1085	99	5
Patient 1	intergenic	intergenic	chr2:90961827	chr2:90973900	DEL	12460	90	4
Patient 1	intergenic	intergenic	chr2:108676900	chr2:108678585	DEL	1550	99	4
Patient 1	intergenic	intergenic	chr2:129354857	chr2:129362738	DEL	7819	80	3
Patient 1	intergenic	intergenic	chr2:130753399	chr2:131846836	INV	1092997	99	3
Patient 1	LOC554226	LOC554226	chr2:132700382	chr2:132704550	DEL	4152	99	5
Patient 1	ERBB4	ERBB4	chr2:213078383	chr2:213079457	DEL	1067	99	5
Patient 1	SCN2A	SPHKAP	chr2:165942586	chr2:228615358	INV	62672456	99	5
Patient 1	SUMF1	SUMF1	chr3:4041892	chr3:4044570	DEL	2676	99	7
Patient 1	intergenic	intergenic	chr3:44716373	chr3:44717472	INV	620	99	3
Patient 1	intergenic	intergenic	chr3:100426477	chr3:100432261	DEL	5751	99	5
Patient 1	COL6A6,DKFZ p667J1615	COL6A6,DK FZp667J161 5	chr3:131830255	chr3:131835903	DEL	5579	81	3
Patient 1	ASTE1	CPNE4	chr3:132226947	chr3:133168666	INV	941230	99	6
Patient 1	intergenic	intergenic	chr3:149962403	chr3:149982092	INV	19226	99	3
Patient 1	intergenic	intergenic	chr3:194227049	chr3:194227721	DEL	571	82	3
Patient 1	intergenic	intergenic	chr4:44202029	chr4:44202514	DEL	497	99	5
Patient 1	GABRG1	GABRG1	chr4:45750718	chr4:45753070	DEL	2245	84	3
Patient 1	intergenic	intergenic	chr4:59626995	chr4:59633268	DEL	6072	99	4
Patient 1	intergenic	intergenic	chr4:64779467	chr4:64780469	DEL	785	99	3
Patient 1	intergenic	intergenic	chr4:83148333	chr4:83150450	DEL	2111	99	4
Patient 1	GRID2	GRID2	chr4:93787462	chr4:93789316	INV	1412	81	2
Patient 1	TBCKL,TBCK	TBCKL,TBC K	chr4:107275986	chr4:107282939	DEL	6815	85	3
Patient 1	NDST4	NDST4	chr4:116148155	chr4:116151439	DEL	3195	99	5
Patient 1	intergenic	intergenic	chr4:126365104	chr4:126379753	ITX	13778	99	7
Patient 1	intergenic	intergenic	chr5:1716615	chr5:1717314	DEL	573	85	3
Patient 1	intergenic	intergenic	chr5:40698394	chr5:40745741	INV	46889	82	2
Patient 1	GHR	GHR	chr5:42664158	chr5:42666970	DEL	2695	99	4
Patient 1	intergenic	intergenic	chr14:60240580	chr5:50234825	CTX	-452	81	4
Patient 1	DAAM1	GPBP1,DKF Zp434G1730	chr14:58804306	chr5:56573012	CTX	-452	99	7
Patient 1	intergenic	intergenic	chr5:143493041	chr5:143494947	DEL	2197	99	4
Patient 1	AK001582	AK001582	chr5:151436608	chr5:151442710	DEL	6057	99	5
Patient 1	FKBP5,AIG6	FKBP5,AIG6	chr6:35734391	chr6:35737880	DEL	3337	87	3
Patient 1	intergenic	intergenic	chr19:32426005	chr6:58887306	ITX	1339	99	90
Patient 1	intergenic	intergenic	chr1:121186860	chr6:58884451	CTX	-452	99	33
Patient 1	intergenic	intergenic	chr6:133383445	chr6:133389630	DEL	6078	84	3
Patient 1	intergenic	intergenic	chr1:121186860	chr7:61606011	CTX	-452	99	45
Patient 1	intergenic	intergenic	chr7:64050788	chr7:64051582	DEL	661	87	3
Patient 1	intergenic	intergenic	chr7:64385761	chr7:64386049	DEL	436	99	4
Patient 1	intergenic	intergenic	chr7:87929200	chr7:87929789	DEL	468	99	6
Patient 1	LOC729156	intergenic	chr7:65934580	chr7:115361372	ITX	49425920	99	6
Patient 1	intergenic	intergenic	chr7:114957232	chr7:114984240	DEL	27002	99	5
Patient 1	BPGM	BPGM	chr7:134000536	chr7:134000978	DEL	461	99	5
Patient 1	intergenic	hTPK1,TPK1	chr7:97231466	chr7:144156757	ITX	46924388	99	4
Patient 1	intergenic	intergenic	chr7:144176367	chr7:144216298	INV	39352	99	5
Patient 1	CNTNAP2	CNTNAP2	chr7:147703639	chr7:147707263	DEL	3513	84	3
Patient 1	intergenic	MLL3	chr7:97190684	chr7:151612557	DEL	54421968	99	4
Patient 1	intergenic	intergenic	chr7:65505879	chr7:155411290	INV	69925744	99	9
Patient 1	intergenic	intergenic	chr7:114976063	chr7:155880974	INV	40904428	99	5
Patient 1	intergenic	intergenic	chr7:114983743	chr7:152070724	INV	37086444	99	8
Patient 1	intergenic	intergenic	chr7:144300234	chr7:152315897	INV	8015244	99	5
Patient 1	intergenic	MLL3	chr7:144303197	chr7:151588622	ITX	7284603	99	5
Patient 1	intergenic	intergenic	chr7:144500244	chr7:152212517	DEL	7712179	99	4
Patient 1	intergenic	DPP6	chr7:149331590	chr7:153421662	INV	4089625	81	2

Patient 1	intergenic	intergenic	chr7:150245097	chr7:155670350	INV	5424755	99	3
Patient 1	intergenic	AX746648	chr7:152335276	chr7:155928781	INV	3593075	99	5
Patient 1	intergenic	intergenic	chr7:152941009	chr7:152941817	DEL	691	84	3
Patient 1	DPP6	DPP6	chr7:154085061	chr7:154086783	DEL	1525	99	4
Patient 1	LMBR1,DIF14, DKFZp547F22 2	LMBR1,DIF1 4,DKFZp547 F222	chr7:156326647	chr7:156351289	DEL	24583	99	5
Patient 1	hTPK1,TPK1	PTPRN2	chr7:144127256	chr7:157251198	INV	13123504	99	7
Patient 1	intergenic	PTPRN2	chr7:144505536	chr7:157357385	INV	12851408	99	5
Patient 1	intergenic	PTPRN2	chr7:144639061	chr7:157060045	INV	12420547	99	3
Patient 1	intergenic	PTPRN2	chr7:150242203	chr7:157057202	DEL	6814883	99	4
Patient 1	intergenic	intergenic	chr7:152297154	chr7:156994237	ITX	4696349	92	3
Patient 1	intergenic	intergenic	chr7:155519909	chr7:156998553	DEL	1478559	99	4
Patient 1	intergenic	PTPRN2	chr7:155598633	chr7:157156664	INV	1557614	99	4
Patient 1	intergenic	intergenic	chr8:20987525	chr8:20988095	DEL	439	89	3
Patient 1	ZMAT4	ZMAT4	chr8:40588775	chr8:40589539	DEL	676	83	3
Patient 1	intergenic	intergenic	chr8:62197911	chr8:62198437	DEL	505	99	6
Patient 1	HFM1	SLCO5A1,O ATPRP4	chr1:91625638	chr8:70764838	CTX	-452	99	78
Patient 1	intergenic	intergenic	chr8:75525382	chr8:75529704	DEL	4113	98	3
Patient 1	CSMD3	CSMD3	chr8:114109608	chr8:114116033	DEL	6341	99	6
Patient 1	intergenic	intergenic	chr8:129831483	chr8:129835219	DEL	3545	96	3
Patient 1	intergenic	intergenic	chr9:25020802	chr9:25021891	DEL	989	83	3
Patient 1	intergenic	intergenic	chr9:67911543	chr9:67919043	INV	7044	98	3
Patient 1	intergenic	intergenic	chr9:77194113	chr9:77201658	DEL	7475	99	5
Patient 1	GNA14	intergenic	chr9:79439711	chr9:84359623	INV	4919418	99	4
Patient 1	GNA14	intergenic	chr9:79440408	chr9:84356340	INV	4915515	97	3
Patient 1	intergenic	intergenic	chr9:84331496	chr9:84360456	DEL	28848	99	4
Patient 1	intergenic	intergenic	chr9:91404689	chr9:91408224	DEL	3451	99	4
Patient 1	intergenic	intergenic	chr9:111325865	chr9:111326670	DEL	640	95	3
Patient 1	intergenic	CTS9,DEC1	chr9:81730353	chr9:117067297	INV	35336448	94	3
Patient 1	CERCAM	ODF2	chr9:130216368	chr9:130260775	DEL	44371	99	4
Patient 1	intergenic	intergenic	chrX:16337615	chrX:16338131	DEL	578	99	5
Patient 1	ADRA1B	intergenic	chr5:159282525	chrX:66899105	CTX	-452	99	17
Patient 1	XAGE3	intergenic	chrX:52908616	chrX:55695700	DEL	2786997	82	3
Patient 1	intergenic	intergenic	chrX:66348190	chrX:66365196	INV	16567	99	3
Patient 1	intergenic	intergenic	chrX:67176277	chrX:67177662	INV	963	99	5
Patient 1	intergenic	intergenic	chr16:33879804	chrY:10653618	CTX	-452	99	9
Patient 1	intergenic	intergenic	chr18:98629	chrY:11920811	CTX	-452	99	8
Patient 1	intergenic	intergenic	chrX:133989152	chrX:133989726	DEL	582	99	7
Patient 1	HSFX1	HSFX1	chrX:148543534	chrX:148638530	INV	94539	99	4
Patient 1	intergenic	intergenic	chrY:57395381	chrY:57400017	ITX	3944	91	3
Patient	Gene1	Gene2	Genome position 1	Genome position 2	Type	Size	Score	Supporting Reads
Patient 2	intergenic	intergenic	chr10:41703468	chr10:41705727	ITX	753	99	11
Patient 2	intergenic	intergenic	chr10:41703468	chr10:41708541	ITX	4242	99	21
Patient 2	intergenic	intergenic	chr10:41703468	chr10:41716990	ITX	12850	99	9
Patient 2	intergenic	intergenic	chr10:41705727	chr10:41715996	DEL	10460	99	24
Patient 2	intergenic	intergenic	chr10:41708541	chr10:41713785	DEL	5147	99	4
Patient 2	intergenic	intergenic	chr10:41705071	chr10:41917212	ITX	211351	92	4
Patient 2	intergenic	intergenic	chr10:41716520	chr10:41916898	DEL	200417	99	6
Patient 2	intergenic	intergenic	chr10:41715996	chr10:41917895	ITX	201147	99	4
Patient 2	intergenic	intergenic	chr10:41716520	chr10:41919258	DEL	203082	99	16
Patient 2	PCDH15	PCDH15	chr10:56437125	chr10:56443302	INV	5658	99	5
Patient 2	intergenic	intergenic	chr10:58182984	chr10:58197075	DEL	13890	93	3
Patient 2	ATAD1	C10orf59	chr10:89503946	chr10:90285606	DEL	781484	87	3
Patient 2	ARHGAP19,F LJ00194	ARHGAP19, FLJ00194	chr10:99024853	chr10:99027423	DEL	2533	99	4
Patient 2	intergenic	DHX32	chr10:89731039	chr10:127573771	INV	37842188	99	4
Patient 2	intergenic	intergenic	chr11:49082201	chr11:49084398	DEL	2056	82	3
Patient 2	intergenic	intergenic	chr11:51125592	chr11:51189138	INV	63097	99	3
Patient 2	intergenic	intergenic	chr11:112122938	chr11:112123378	DEL	449	99	4
Patient 2	TSPAN9	TSPAN9	chr12:3177169	chr12:3178320	DEL	1131	99	5

Patient 2	intergenic	ABCC9	chr12:8187286	chr12:21918557	ITX	13730511	99	4
Patient 2	intergenic	intergenic	chr12:10345765	chr12:24764410	ITX	14417851	99	4
Patient 2	CDA14,ERGIC 2	OVCH1	chr12:29406022	chr12:29482789	INV	76319	90	3
Patient 2	CDA14,ERGIC 2	FAM60A	chr12:29420256	chr12:31326580	INV	1905785	99	7
Patient 2	intergenic	intergenic	chr12:8194425	chr12:39103739	ITX	30908546	99	4
Patient 2	intergenic	intergenic	chr12:39092571	chr12:39136638	INV	43597	99	4
Patient 2	intergenic	intergenic	chr12:129932724	chr12:129933306	DEL	577	99	5
Patient 2	EPSTI1	EPSTI1	chr13:42437632	chr13:42439491	DEL	1691	85	3
Patient 2	intergenic	intergenic	chr13:110502424	chr13:110502939	DEL	400	99	6
Patient 2	hADV29S1,AV 4S1,hADV36S 1,TRA@,AK09 3552,TCR-alpha,hADV38 S2,TRD,AV30 S1,TCRA	hADV29S1,A V4S1,hADV 36S1,TRA@ ,AK093552,T CR-alpha,hADV 38S2,AV30S 1,TRD,TCR A	chr14:21951500	chr14:21952125	DEL	565	99	5
Patient 2	abParts	abParts	chr14:105762282	chr14:106253760	ITX	490794	99	4
Patient 2	SNRPN	SNRPN	chr15:22668011	chr15:22669901	DEL	1779	99	5
Patient 2	intergenic	GABRG3	chr15:23953281	chr15:24854871	DEL	901465	99	8
Patient 2	intergenic	GABRG3	chr15:24157218	chr15:24855727	ITX	697612	99	4
Patient 2	intergenic	intergenic	chr16:13201970	chr16:13204036	DEL	2045	99	4
Patient 2	intergenic	intergenic	chr16:44949805	chr16:44985797	INV	35410	99	5
Patient 2	intergenic	intergenic	chr16:33281489	chr16:33287013	DEL	5396	99	5
Patient 2	intergenic	intergenic	chr16:33827377	chr16:33890851	INV	63444	82	3
Patient 2	intergenic	intergenic	chr16:33894555	chr16:33895597	DEL	1009	99	4
Patient 2	HYDIN	KIAA1864,H YDIN	chr16:69535296	chr16:69537302	DEL	2127	99	7
Patient 2	intergenic	intergenic	chr16:83746241	chr16:83747143	INV	415	99	5
Patient 2	KCTD11	intergenic	chr17:7198299	chr17:14991191	DEL	7792890	99	6
Patient 2	intergenic	intergenic	chr17:23804466	chr17:23807680	DEL	3132	99	6
Patient 2	WIRE,WIPF2	WIRE,WIPF 2	chr17:35631361	chr17:35631965	DEL	480	99	4
Patient 2	intergenic	intergenic	chr17:38793367	chr17:38795793	DEL	2222	93	3
Patient 2	intergenic	intergenic	chr17:59566755	chr17:59567882	DEL	994	99	5
Patient 2	intergenic	ROCK1	chr18:98051	chr18:100781	ITX	1382	99	8
Patient 2	SPIRE1	SPIRE1	chr18:12493608	chr18:12494445	DEL	752	99	6
Patient 2	KIAA1881	KIAA1881	chr19:4462123	chr19:4462725	DEL	415	99	4
Patient 2	intergenic	intergenic	chr19:14823940	chr19:14875121	ITX	50334	99	4
Patient 2	BC082233,ZN F681	BC082233,Z NF681	chr19:23727631	chr19:23728170	ITX	-437	99	6
Patient 2	intergenic	intergenic	chr19:32571791	chr19:32572528	DEL	534	99	4
Patient 2	NPAS1	NPAS1	chr19:52220079	chr19:52220762	DEL	484	82	3
Patient 2	intergenic	intergenic	chr1:24392836	chr1:24396307	DEL	3337	99	4
Patient 2	BMP8A	BMP8A	chr1:39742691	chr1:39742928	ITX	-443	99	4
Patient 2	intergenic	intergenic	chr19:32424642	chr1:121185264	CTX	-453	99	2137
Patient 2	intergenic	intergenic	chr19:32426352	chr1:121185264	CTX	-453	99	152
Patient 2	intergenic	intergenic	chr19:32428642	chr1:121185264	CTX	-453	99	25
Patient 2	intergenic	intergenic	chr19:32430529	chr1:121185264	CTX	-453	99	186
Patient 2	intergenic	intergenic	chr17:22177424	chr1:121057222	CTX	-453	99	7
Patient 2	intergenic	intergenic	chr1:121087915	chr1:121184274	DEL	96143	96	3
Patient 2	DKFZp451B14 18,AK023548, KIAA1693,NB PF1,NBPF12, AK023809	DKFZp451B 1418,KIAA1 693,NBPF1, NBPF12	chr1:146219590	chr1:146242542	INV	22463	99	4
Patient 2	IQGAP3	IQGAP3	chr1:154793294	chr1:154795572	DEL	2264	99	8
Patient 2	intergenic	intergenic	chr1:169051570	chr1:169053111	DEL	1327	95	3
Patient 2	intergenic	intergenic	chr1:185982558	chr1:185989171	DEL	6459	99	5
Patient 2	intergenic	intergenic	chr1:196023591	chr1:196024513	INV	694	99	6
Patient 2	intergenic	intergenic	chr1:234615592	chr1:234617954	DEL	2223	80	3

Patient 2	intergenic	intergenic	chr20:7346672	chr20:7351618	DEL	4882	99	7
Patient 2	intergenic	intergenic	chr20:26152521	chr20:26153460	DEL	771	99	4
Patient 2	intergenic	intergenic	chr21:9727541	chr21:9729213	ITX	-400	99	6
Patient 2	intergenic	intergenic	chr21:9733989	chr21:9734632	DEL	677	99	12
Patient 2	intergenic	intergenic	chr21:9755654	chr21:9756341	DEL	553	99	4
Patient 2	intergenic	intergenic	chr21:9771834	chr21:9773712	DEL	2229	99	5
Patient 2	intergenic	intergenic	chr21:9779560	chr21:9779726	DEL	405	97	4
Patient 2	intergenic	intergenic	chr21:9788494	chr21:9794700	DEL	6041	99	6
Patient 2	intergenic	intergenic	chr21:23296664	chr21:23297360	DEL	640	99	5
Patient 2	intergenic	intergenic	chr21:26942861	chr21:26943482	INV	557	99	6
Patient 2	intergenic	intergenic	chr21:29474094	chr21:29474550	DEL	400	99	4
Patient 2	TMPRSS2	TMPRSS2	chr21:41791756	chr21:41792245	DEL	415	99	4
Patient 2	APOL3	APOL1	chr22:34868369	chr22:34989013	INV	120128	99	4
Patient 2	SNTG2	SNTG2	chr2:1337021	chr2:1337461	DEL	463	99	5
Patient 2	intergenic	intergenic	chr2:2777640	chr2:2778251	DEL	456	99	4
Patient 2	intergenic	AK001558	chr2:4276977	chr2:12083409	INV	7805933	96	3
Patient 2	CLIP4,DKFZp 761O0610	CLIP4,DKFZ p761O0610	chr2:29245603	chr2:29256710	DEL	11637	87	4
Patient 2	intergenic	intergenic	chr2:21185711	chr2:49609376	DEL	28423648	99	5
Patient 2	BIRC6	intergenic	chr2:32615613	chr2:51223821	INV	18607748	93	3
Patient 2	CAPN13	intergenic	chr2:30807292	chr2:77650775	INV	46842956	95	3
Patient 2	intergenic	CTNNA2	chr2:4851215	chr2:79723311	DEL	74872056	96	4
Patient 2	intergenic	intergenic	chr2:41875462	chr2:79091919	ITX	37215720	82	3
Patient 2	intergenic	CTNNA2	chr2:79022836	chr2:80418167	DEL	1395233	80	3
Patient 2	intergenic	BC031698,B X648045,AL 137717	chr2:15203860	chr2:88864772	INV	73660504	90	3
Patient 2	intergenic	intergenic	chr2:90961239	chr2:90976498	DEL	15631	99	6
Patient 2	intergenic	intergenic	chr2:91654803	chr2:91664825	ITX	9290	99	4
Patient 2	intergenic	intergenic	chr2:175920790	chr2:175952680	INV	31418	99	4
Patient 2	GIGYF2	intergenic	chr2:233378697	chr2:236012299	DEL	2633515	99	4
Patient 2	intergenic	intergenic	chr2:239165106	chr2:239166467	DEL	1316	99	6
Patient 2	LOC643905	LOC643905	chr2:240630071	chr2:240630754	DEL	508	99	4
Patient 2	intergenic	intergenic	chr3:5510388	chr3:5514280	DEL	3915	98	4
Patient 2	AF279782	AF279782	chr3:6675779	chr3:6676399	DEL	417	99	4
Patient 2	BC020876	BC020876	chr3:8428451	chr3:8429448	DEL	836	83	3
Patient 2	CCDC123	intergenic	chr19:38136308	chr3:76066253	CTX	-453	95	5
Patient 2	intergenic	intergenic	chr3:112726238	chr3:112731686	DEL	5323	99	4
Patient 2	intergenic	CPNE4	chr3:131534792	chr3:132847518	DEL	1312684	99	4
Patient 2	PCCB	PCCB	chr3:137503645	chr3:137508897	DEL	5223	95	4
Patient 2	intergenic	intergenic	chr3:147127656	chr3:147131913	DEL	4234	99	5
Patient 2	intergenic	intergenic	chr3:149961682	chr3:149982161	INV	20068	86	3
Patient 2	intergenic	AF388367	chr3:145169955	chr3:152177845	INV	7007412	87	3
Patient 2	PLCH1	intergenic	chr3:156768926	chr3:169469669	DEL	12700604	83	3
Patient 2	FKSG52	BCL6	chr3:48212983	chr3:188936489	INV	140723040	99	5
Patient 2	intergenic	BCL6	chr3:72982754	chr3:188930982	ITX	115947416	99	5
Patient 2	intergenic	intergenic	chr3:197211953	chr3:198849472	DEL	1637342	94	3
Patient 2	intergenic	intergenic	chr4:3786323	chr4:3786551	ITX	-430	82	3
Patient 2	intergenic	intergenic	chr4:11762925	chr4:11766305	DEL	3354	99	7
Patient 2	intergenic	intergenic	chr4:48804751	chr4:48817999	ITX	12080	99	5
Patient 2	intergenic	intergenic	chr4:109940512	chr4:109941678	DEL	1166	99	5
Patient 2	intergenic	intergenic	chr4:164344399	chr4:164344921	DEL	446	99	6
Patient 2	intergenic	intergenic	chr4:180334764	chr4:180335555	DEL	662	81	3
Patient 2	intergenic	intergenic	chr4:189427229	chr4:189428067	DEL	611	98	3
Patient 2	intergenic	intergenic	chr5:10326271	chr5:10328376	DEL	1884	96	3
Patient 2	intergenic	intergenic	chr5:53158502	chr5:53161649	INV	2683	98	3
Patient 2	ADCY2	PDE4D	chr5:7834606	chr5:58873133	INV	51038084	99	5
Patient 2	ADCY2	PDE4D	chr5:7834606	chr5:58902995	INV	51067996	99	6
Patient 2	CMYA5	CMYA5	chr5:79085496	chr5:79087614	ITX	1408	91	3
Patient 2	intergenic	intergenic	chr5:143492701	chr5:143495527	ITX	1618	99	11
Patient 2	intergenic	intergenic	chr5:150157696	chr5:150161847	DEL	3962	99	4
Patient 2	intergenic	intergenic	chr5:169530259	chr5:169531618	INV	915	99	3

Patient	Gene1	Gene2	Genomic position 1	Genomic position 2	Type	Size	Score	Supporting Reads
Patient 2	ZNF346	ZNF346	chr5:176427646	chr5:176429035	DEL	1231	84	3
Patient 2	AK094934	FARS2	chr6:4952401	chr6:5376741	DEL	424200	99	4
Patient 2	intergenic	intergenic	chr6:14853153	chr6:14853698	DEL	429	99	4
Patient 2	AK026189,BC 044235	AK026189,B C044235	chr6:22160607	chr6:22161753	DEL	981	85	3
Patient 2	FAM65B	FAM65B	chr6:24919855	chr6:24925979	DEL	6094	99	5
Patient 2	C6orf142	C6orf142	chr6:54036661	chr6:54042853	DEL	5982	96	3
Patient 2	intergenic	intergenic	chr10:41720220	chr6:58887315	ITX	1011	99	41
Patient 2	intergenic	intergenic	chr1:121186863	chr6:58884224	CTX	-453	99	57
Patient 2	intergenic	intergenic	chr6:67065447	chr6:67105758	DEL	40213	99	4
Patient 2	C6orf204	C6orf204	chr6:119118405	chr6:119120979	ITX	1282	99	10
Patient 2	intergenic	intergenic	chr6:161646307	chr6:161647837	DEL	1581	99	6
Patient 2	SMOC2	SMOC2	chr6:168633303	chr6:168633535	ITX	-427	99	5
Patient 2	SMOC2	SMOC2	chr6:168704086	chr6:168705965	DEL	1751	99	8
Patient 2	TRGC2	AMPH	chr7:38263752	chr7:38590279	INV	326068	99	5
Patient 2	intergenic	intergenic	chr7:39512891	chr7:39518366	DEL	5493	98	4
Patient 2	intergenic	intergenic	chr7:57969686	chr7:57978953	DEL	9417	97	4
Patient 2	intergenic	intergenic	chr1:121186863	chr7:61606004	CTX	-453	99	118
Patient 2	intergenic	intergenic	chr7:61606004	chr7:61607905	ITX	811	99	138
Patient 2	intergenic	intergenic	chr1:121186863	chr7:61607699	CTX	-453	89	10
Patient 2	intergenic	intergenic	chr7:100787934	chr7:100790523	DEL	2557	99	6
Patient 2	CAV1,DQ6560 15,CAV2,EF07 0122,EF07011 9,EF070117	CAV1,DQ65 6015,CAV2, EF070122,E F070119,EF 070117	chr7:115718797	chr7:115728493	DEL	9634	99	4
Patient 2	SVOPL	SVOPL	chr7:137946944	chr7:137947834	DEL	797	99	5
Patient 2	intergenic	intergenic	chr7:144547890	chr7:144552351	DEL	4555	99	5
Patient 2	HTR5A	intergenic	chr7:154507591	chr7:154512133	ITX	3155	90	4
Patient 2	PTPRN2	PTPRN2	chr7:157739304	chr7:157740098	DEL	768	99	7
Patient 2	POLR2L	ChGn,CSGA LNACT1	chr11:830024	chr8:19477102	CTX	-453	94	6
Patient 2	intergenic	intergenic	chr8:1097364	chr8:29996220	DEL	28898770	99	6
Patient 2	intergenic	intergenic	chr8:40408861	chr8:40415495	DEL	6543	99	5
Patient 2	NKAIN3	NKAIN3	chr8:63586542	chr8:63587586	DEL	949	99	5
Patient 2	EYA1	EYA1	chr8:72377057	chr8:72380377	DEL	3103	97	3
Patient 2	IMPA1	DKFZp779L 1068	chr8:58068392	chr8:94087312	DEL	36018744	90	3
Patient 2	DKFZp779L10 68	intergenic	chr8:94087089	chr8:102100366	DEL	8013266	99	8
Patient 2	intergenic	intergenic	chr8:128008551	chr8:128357925	ITX	348601	99	5
Patient 2	C9orf93	C9orf93	chr9:15805068	chr9:15811939	DEL	6662	99	5
Patient 2	intergenic	intergenic	chr9:44682156	chr9:46976011	INV	2293384	99	3
Patient 2	CR627148	intergenic	chr9:66201970	chr9:66214090	INV	11603	87	3
Patient 2	intergenic	intergenic	chr9:91365837	chr9:91367853	DEL	1946	99	8
Patient 2	OATPP4,SL CO5A1	intergenic	chr8:70765046	chrX:108184244	CTX	-453	99	8
Patient 2	intergenic	intergenic	chrX:133989177	chrX:133989744	DEL	574	99	4
Patient 2	ROCK1	intergenic	chr18:100781	chrY:11939552	CTX	-453	99	8
Patient 2	intergenic	intergenic	chr4:191152167	chrY:10570265	CTX	-453	99	6
Patient 2	BAGE2,BAGE 5	intergenic	chr21:10076484	chrY:57410468	CTX	-453	99	7
Patient 2	intergenic	intergenic	chrY:57393478	chrY:57400159	ITX	5877	99	6
Patient 2	intergenic	intergenic	chrY:57393737	chrY:57400471	DEL	6743	99	15
Patient 2	intergenic	intergenic	chrY:57395349	chrY:57400159	ITX	3975	99	8
Patient	Gene1	Gene2	Genomic position 1	Genomic position 2	Type	Size	Score	Supporting Reads
Patient 3	AGRN	AGRN	chr1:955863	chr1:956322	DEL	644	99	14
Patient 3	intergenic	intergenic	chr1:1856236	chr1:1856839	DEL	730	99	12
Patient 3	WDR8	WDR8	chr1:3550024	chr1:3550756	DEL	636	99	5
Patient 3	CAMTA1	CAMTA1	chr1:7492630	chr1:7494171	DEL	1502	99	6
Patient 3	intergenic	intergenic	chr1:30511128	chr1:30511856	DEL	1393	99	8
Patient 3	intergenic	intergenic	chr1:121059454	chr1:121186955	ITX	125580	99	7

Patient 3	intergenic	CR936796,L OC375010	chr1:141483875	chr1:141909258	INV	424654	99	5
Patient 3	NBPF20,PDE4, DIP,KIAA1245, NBPF8,NBPF1 4,NBPF10	NBPF20,PD E4DIP,KIAA 1245,NBPF8 ,NBPF14,NB PF10	chr1:143605516	chr1:143606579	DEL	1078	99	8
Patient 3	NBPF20,PDE4, DIP,KIAA1245, NBPF8,NBPF1 4,NBPF10	NBPF20,PD E4DIP,KIAA 1245,NBPF8 ,NBPF14,NB PF10	chr1:143607983	chr1:143618189	DEL	10427	99	8
Patient 3	NBPF20,KIAA 1693	NBPF20,KIA A1693	chr1:147114873	chr1:147117199	DEL	853	99	20
Patient 3	intergenic	intergenic	chr1:151482394	chr1:151483061	DEL	585	99	7
Patient 3	AK125248	intergenic	chr1:715058	chr1:222268848	ITX	221553024	99	5
Patient 3	intergenic	intergenic	chr1:225052022	chr1:225052651	DEL	480	99	8
Patient 3	C1orf71	C1orf71	chr1:244849835	chr1:244850441	DEL	461	99	5
Patient 3	intergenic	intergenic	chr2:898643	chr2:899539	DEL	742	99	7
Patient 3	TPO	TPO	chr2:1439469	chr2:1440123	DEL	670	99	9
Patient 3	intergenic	intergenic	chr2:10070514	chr2:10073172	ITX	1285	99	10
Patient 3	intergenic	intergenic	chr2:11911569	chr2:11912405	DEL	726	99	5
Patient 3	LTBP1	LTBP1	chr2:33077877	chr2:33080801	DEL	2925	99	6
Patient 3	BCL11A	BCL11A	chr2:60547705	chr2:60548433	DEL	647	99	9
Patient 3	intergenic	intergenic	chr2:88356842	chr2:88358818	INV	1083	99	7
Patient 3	intergenic	intergenic	chr2:88603391	chr2:88603615	DEL	623	99	5
Patient 3	intergenic	intergenic	chr2:91654669	chr2:91664912	ITX	9148	99	10
Patient 3	4-Mar	4-Mar	chr2:216866503	chr2:216867056	DEL	500	99	6
Patient 3	SP140L	SP140L	chr2:230915909	chr2:230916195	DEL	689	99	5
Patient 3	HDAC4	HDAC4	chr2:23987582	chr2:239868068	DEL	484	99	14
Patient 3	intergenic	intergenic	chr2:240890524	chr2:240891100	DEL	488	99	10
Patient 3	intergenic	intergenic	chr2:241228125	chr2:241228458	DEL	777	99	10
Patient 3	intergenic	intergenic	chr2:241435859	chr2:241436821	DEL	731	99	6
Patient 3	intergenic	intergenic	chr2:242409902	chr2:242410953	DEL	902	99	15
Patient 3	AK126307	AK126307	chr3:636737	chr3:636934	DEL	453	99	5
Patient 3	PTPRG	PTPRG	chr3:61833716	chr3:61835977	INV	1776	99	6
Patient 3	CADPS	BC039502,B C043407	chr3:62650816	chr3:63021751	DEL	370965	99	6
Patient 3	intergenic	intergenic	chr3:68822377	chr3:68830658	DEL	8249	99	5
Patient 3	intergenic	intergenic	chr3:76862098	chr3:76862826	DEL	581	99	6
Patient 3	intergenic	intergenic	chr3:120902525	chr3:120903097	DEL	519	99	5
Patient 3	ZPLD1	intergenic	chr3:103450174	chr3:188375770	DEL	84925480	99	6
Patient 3	intergenic	intergenic	chr3:158858494	chr3:188364265	INV	29505546	99	8
Patient 3	intergenic	intergenic	chr3:196705480	chr3:196706234	DEL	910	99	6
Patient 3	MUC4	MUC4	chr3:196992153	chr3:196995052	DEL	3396	99	6
Patient 3	MUC4	MUC4	chr3:196994762	chr3:196995052	DEL	856	94	5
Patient 3	MUC4	MUC4	chr3:196997505	chr3:196999439	DEL	1908	99	7
Patient 3	TNK2	TNK2	chr3:197085869	chr3:197086684	DEL	655	99	6
Patient 3	intergenic	intergenic	chr3:197138798	chr3:197139794	DEL	1085	99	6
Patient 3	BC071730	BC071730	chr3:197172709	chr3:197173646	DEL	815	99	5
Patient 3	intergenic	intergenic	chr3:197310192	chr3:197310942	DEL	827	99	16
Patient 3	intergenic	intergenic	chr4:3535671	chr4:3536344	DEL	767	99	6
Patient 3	GRXCR1	GRXCR1	chr4:42599906	chr4:42600782	DEL	801	99	6
Patient 3	intergenic	intergenic	chr1:142120283	chr4:49207015	CTX	-488	99	73
Patient 3	intergenic	intergenic	chr4:48805575	chr4:48815776	DEL	10265	99	13
Patient 3	intergenic	intergenic	chr4:48844595	chr4:48849742	DEL	5336	99	5
Patient 3	intergenic	intergenic	chr4:49329038	chr4:49340186	DEL	2364	99	6
Patient 3	intergenic	intergenic	chr4:89139787	chr4:89140457	DEL	579	99	5
Patient 3	intergenic	intergenic	chr4:189427240	chr4:189427901	DEL	517	99	6
Patient 3	intergenic	intergenic	chr4:190392173	chr4:190393202	DEL	854	99	15
Patient 3	intergenic	intergenic	chr4:190809811	chr4:190810558	DEL	653	99	8
Patient 3	intergenic	intergenic	chr4:190823308	chr4:190850847	INV	26840	99	49
Patient 3	intergenic	intergenic	chr4:190893535	chr4:190894464	DEL	927	99	10

Patient 3	LOC728613	LOC728613	chr5:1680140	chr5:1681863	DEL	1766	99	5
Patient 3	intergenic	intergenic	chr5:8373476	chr5:8374632	DEL	1218	99	5
Patient 3	intergenic	intergenic	chr5:8990782	chr5:8991842	DEL	1037	99	5
Patient 3	intergenic	intergenic	chr5:10326280	chr5:10328372	DEL	1964	99	13
Patient 3	CTNND2	CTNND2	chr5:11869768	chr5:11870573	DEL	595	99	5
Patient 3	intergenic	intergenic	chr5:30951198	chr5:30951955	DEL	635	99	5
Patient 3	HCN1	HCN1	chr5:45562696	chr5:45563234	DEL	581	99	10
Patient 3	intergenic	intergenic	chr5:57895183	chr5:57895774	DEL	573	99	11
Patient 3	CSF1R	CSF1R	chr5:149421904	chr5:149422436	DEL	508	99	9
Patient 3	intergenic	intergenic	chr5:158954806	chr5:158955572	DEL	739	99	9
Patient 3	intergenic	intergenic	chr5:169530266	chr5:169531747	INV	621	99	10
Patient 3	intergenic	intergenic	chr6:29793427	chr6:29796081	DEL	2659	99	6
Patient 3	intergenic	intergenic	chr6:29923031	chr6:29923489	DEL	597	99	13
Patient 3	HLA-A*0226,AK097 625	HLA-A*0226,AK0 97625	chr6:30007755	chr6:30009502	DEL	1794	99	15
Patient 3	intergenic	intergenic	chr6:31319594	chr6:31321286	DEL	1611	99	9
Patient 3	intergenic	intergenic	chr6:32886790	chr6:32887794	DEL	1144	99	7
Patient 3	ZFAND3	ZFAND3	chr6:37959190	chr6:37960599	DEL	1394	99	5
Patient 3	COLA1L,COL2 1A1	COLA1L,CO L2A1	chr6:56178131	chr6:56186614	DEL	8605	99	5
Patient 3	intergenic	intergenic	chr1:121056506	chr6:58887316	ITX	655	99	332
Patient 3	intergenic	intergenic	chr6:74670297	chr6:74677202	DEL	6924	99	12
Patient 3	C6orf204	C6orf204	chr6:119119403	chr6:119120731	DEL	1693	98	5
Patient 3	DACT2	DACT2	chr6:168459844	chr6:168461634	DEL	1665	99	7
Patient 3	FAM120B	FAM120B	chr6:170549990	chr6:170551033	DEL	867	99	7
Patient 3	intergenic	intergenic	chr7:319338	chr7:321076	DEL	1774	99	9
Patient 3	PRKAR1B	PRKAR1B	chr7:572831	chr7:573562	DEL	509	99	7
Patient 3	HEATR2,DKF Zp762F1415	HEATR2,DK FzP762F141 5	chr7:753890	chr7:754430	DEL	514	99	12
Patient 3	EIF3B	EIF3B	chr7:2383712	chr7:2384362	DEL	652	99	8
Patient 3	SDK1	SDK1	chr7:3969104	chr7:3969882	DEL	623	99	11
Patient 3	intergenic	intergenic	chr7:24224600	chr7:24225040	DEL	481	99	6
Patient 3	intergenic	intergenic	chr7:50235431	chr7:50236199	INV	413	99	7
Patient 3	EGFR	EGFR	chr7:55202204	chr7:55202616	ITX	-427	99	6
Patient 3	intergenic	intergenic	chr6:58887316	chr7:61605327	CTX	-488	99	303
Patient 3	intergenic	intergenic	chr7:61463839	chr7:61464631	DEL	618	99	6
Patient 3	intergenic	intergenic	chr7:62023386	chr7:62084042	ITX	59651	99	8
Patient 3	AUTS2	AUTS2	chr7:69598570	chr7:69600282	DEL	779	99	10
Patient 3	ABCB1,RUND C3B,mdr1	ABCB1,RUN DC3B,mdr1	chr7:87146262	chr7:87148728	DEL	2813	99	7
Patient 3	HTR5A	intergenic	chr7:154507557	chr7:154512125	ITX	3052	99	10
Patient 3	PTPRN2	PTPRN2	chr7:157426205	chr7:157426863	DEL	612	99	8
Patient 3	PTPRN2	PTPRN2	chr7:157739376	chr7:157740085	DEL	827	99	15
Patient 3	PTPRN2	PTPRN2	chr7:157817185	chr7:157819118	ITX	1097	99	5
Patient 3	PTPRN2	PTPRN2	chr7:157978813	chr7:157979271	DEL	452	99	15
Patient 3	VIPR2	VIPR2	chr7:158575625	chr7:158576456	DEL	675	99	6
Patient 3	intergenic	intergenic	chr7:158691562	chr7:158692277	DEL	751	99	6
Patient 3	intergenic	intergenic	chr7:158810114	chr7:158815575	DEL	5395	99	8
Patient 3	BC038783,BC 022082	BC038783,B C022082	chr8:951028	chr8:955047	DEL	3818	99	6
Patient 3	BC022082	BC022082	chr8:976876	chr8:977386	DEL	498	99	11
Patient 3	intergenic	intergenic	chr8:34665529	chr8:34666622	INV	907	98	5
Patient 3	intergenic	intergenic	chr8:34871725	chr8:34883816	INV	11738	99	5
Patient 3	intergenic	intergenic	chr8:58280848	chr8:58290328	ITX	8678	99	7
Patient 3	intergenic	intergenic	chr8:58285560	chr8:58290207	DEL	4468	99	8
Patient 3	intergenic	intergenic	chr8:61367490	chr8:61367916	DEL	470	99	6
Patient 3	intergenic	intergenic	chr8:62197859	chr8:62198455	DEL	634	99	8
Patient 3	intergenic	intergenic	chr8:75252290	chr8:75258391	INV	7007	99	35
Patient 3	intergenic	intergenic	chr8:86027879	chr8:86037381	INV	8319	99	7
Patient 3	intergenic	intergenic	chr8:96944333	chr8:96948764	DEL	4438	99	6

Patient 3	SDC2	SDC2	chr8:97589869	chr8:97591125	DEL	1245	99	7
Patient 3	intergenic	intergenic	chr8:110303786	chr8:110304225	DEL	465	99	9
Patient 3	intergenic	intergenic	chr8:126750535	chr8:126750881	DEL	477	99	7
Patient 3	intergenic	intergenic	chr8:127261383	chr8:127263750	DEL	2428	99	27
Patient 3	intergenic	intergenic	chr8:142426745	chr8:142428412	DEL	477	99	16
Patient 3	FLJ43860	FLJ43860	chr8:142571737	chr8:142572332	DEL	599	99	10
Patient 3	intergenic	intergenic	chr8:142950743	chr8:142951261	DEL	714	99	7
Patient 3	intergenic	intergenic	chr8:144127827	chr8:144128521	DEL	530	99	8
Patient 3	intergenic	intergenic	chr8:144819244	chr8:144820299	DEL	933	99	8
Patient 3	intergenic	intergenic	chr8:145616353	chr8:145618367	DEL	2014	99	9
Patient 3	PRG-3	PRG-3	chr9:102904184	chr9:102910294	DEL	6050	99	6
Patient 3	intergenic	intergenic	chr9:138646413	chr9:138646940	DEL	592	99	8
Patient 3	ADARB2	ADARB2	chr10:1372347	chr10:1373030	DEL	575	99	6
Patient 3	ADARB2	ADARB2	chr10:1649237	chr10:1649878	DEL	517	99	18
Patient 3	intergenic	intergenic	chr10:11447787	chr10:11448656	DEL	915	99	14
Patient 3	intergenic	intergenic	chr10:28690453	chr10:28691201	DEL	613	99	6
Patient 3	intergenic	intergenic	chr10:28703799	chr10:28705134	DEL	1346	99	5
Patient 3	intergenic	intergenic	chr1:121186859	chr10:41849268	CTX	-488	99	20
Patient 3	intergenic	intergenic	chr2:90960493	chr10:41705648	ITX	-403	99	13
Patient 3	intergenic	intergenic	chr10:41705648	chr10:41712639	DEL	7064	99	12
Patient 3	intergenic	intergenic	chr10:41676456	chr10:41676777	DEL	1214	99	12
Patient 3	intergenic	intergenic	chr10:41678235	chr10:41683585	ITX	3226	99	7
Patient 3	intergenic	AK098044,P ARG	chr10:47124383	chr10:51159029	INV	4034255	99	8
Patient 3	intergenic	intergenic	chr10:60872657	chr10:60873537	DEL	893	99	6
Patient 3	FER1L3,MYO F	FER1L3,MY OF	chr10:95196963	chr10:95199413	DEL	2400	99	6
Patient 3	BC040734	INA	chr10:104981208	chr10:105040024	DEL	58768	99	5
Patient 3	ADAM12	ADAM12	chr10:127735183	chr10:127735971	DEL	874	99	17
Patient 3	intergenic	intergenic	chr10:132048367	chr10:132048943	DEL	472	99	5
Patient 3	TCERG1L	TCERG1L	chr10:132977753	chr10:132978420	DEL	456	99	6
Patient 3	intergenic	intergenic	chr10:133580556	chr10:133581366	DEL	846	99	13
Patient 3	KIAA1674,LR RC27	KIAA1674,L RRC27	chr10:134015548	chr10:134016282	DEL	738	99	5
Patient 3	AK310947	AK310947	chr10:134577561	chr10:134578315	DEL	560	99	9
Patient 3	KNDC1	KNDC1	chr10:134885991	chr10:134886907	DEL	708	99	5
Patient 3	MUC6	MUC6	chr11:1006607	chr11:1007979	ITX	449	99	9
Patient 3	intergenic	intergenic	chr11:1872383	chr11:1893537	DEL	21713	99	8
Patient 3	intergenic	intergenic	chr11:25520939	chr11:25521418	DEL	495	99	7
Patient 3	intergenic	intergenic	chr11:50404462	chr11:50411204	ITX	5718	92	5
Patient 3	intergenic	intergenic	chr11:60622987	chr11:60625015	ITX	-451	99	21
Patient 3	intergenic	intergenic	chr11:60625111	chr11:60625443	DEL	590	99	22
Patient 3	ARHGAP20	ARHGAP20	chr11:109994683	chr11:109995202	DEL	548	99	18
Patient 3	GRIK4	GRIK4	chr11:119892836	chr11:119893587	DEL	834	99	10
Patient 3	intergenic	intergenic	chr11:128187924	chr11:128188916	DEL	805	99	6
Patient 3	intergenic	intergenic	chr12:9449058	chr12:9449987	DEL	988	99	7
Patient 3	intergenic	intergenic	chr12:15909862	chr12:15912936	DEL	3104	89	5
Patient 3	intergenic	intergenic	chr12:24832106	chr12:24832960	DEL	799	99	8
Patient 3	intergenic	intergenic	chr12:39161016	chr12:39162245	DEL	1748	99	13
Patient 3	intergenic	intergenic	chr12:39163196	chr12:39164072	DEL	950	99	7
Patient 3	intergenic	intergenic	chr12:39162245	chr12:39165167	ITX	1883	99	11
Patient 3	TMEM120B	TMEM120B	chr12:120669596	chr12:120670325	DEL	618	99	5
Patient 3	TMEM132D	TMEM132D	chr12:128138400	chr12:128140060	DEL	1466	99	6
Patient 3	RIMBP2	RIMBP2	chr12:129697902	chr12:129699817	DEL	2071	98	5
Patient 3	intergenic	intergenic	chr12:131470824	chr12:131471419	DEL	632	99	11
Patient 3	intergenic	intergenic	chr12:131560028	chr12:131560633	DEL	759	99	11
Patient 3	ANKLE2	ANKLE2	chr12:131818859	chr12:131819556	DEL	841	99	16
Patient 3	intergenic	intergenic	chr13:21421487	chr13:21421783	DEL	455	99	10
Patient 3	intergenic	intergenic	chr13:22386058	chr13:23800225	ITX	1256138	99	9
Patient 3	intergenic	intergenic	chr13:25948044	chr13:25950267	DEL	2209	99	15
Patient 3	HMGB1	HMGB1	chr13:30073591	chr13:30073920	DEL	468	99	13
Patient 3	intergenic	intergenic	chr13:35689949	chr13:35693579	ITX	2679	95	5

Patient 3	pp13759	pp13759	chr13:44853684	chr13:44854279	DEL	703	99	11
Patient 3	IRS2	IRS2	chr13:109216272	chr13:109217124	DEL	1124	99	24
Patient 3	COL4A2	COL4A2	chr13:109930775	chr13:109932771	DEL	659	99	18
Patient 3	FAM70B	FAM70B	chr13:113607446	chr13:113608435	DEL	1049	99	5
Patient 3	FAM70B	FAM70B	chr13:113620391	chr13:113620826	DEL	481	99	13
Patient 3	RASA3	RASA3	chr13:113903717	chr13:113904225	DEL	562	99	9
Patient 3	abParts	abParts	chr14:105520006	chr14:105521963	DEL	1857	99	5
Patient 3	abParts	abParts	chr14:105762098	chr14:106253994	ITX	490747	99	7
Patient 3	abParts	abParts	chr14:106003474	chr14:106245024	ITX	240814	99	5
Patient 3	intergenic	intergenic	chr15:20374564	chr15:20377244	ITX	1675	99	6
Patient 3	DKFZp451C02 3,SRL	DKFZp451C 023,SRL	chr16:4191407	chr16:4191770	DEL	479	99	9
Patient 3	intergenic	intergenic	chr16:11591270	chr16:11592791	DEL	1617	99	5
Patient 3	intergenic	intergenic	chr16:21502802	chr16:22618257	INV	1115765	99	6
Patient 3	AQP8	AQP8	chr16:25137547	chr16:25138715	DEL	1180	99	5
Patient 3	intergenic	intergenic	chr16:44952561	chr16:44985964	INV	32102	99	7
Patient 3	intergenic	intergenic	chr16:44952561	chr16:44957505	DEL	5310	99	8
Patient 3	WWP2	WWP2	chr16:68412246	chr16:68416732	ITX	3356	91	5
Patient 3	intergenic	intergenic	chr16:73028502	chr16:73029204	DEL	825	99	9
Patient 3	KIAA1879,PK D1L2	KIAA1879,P KD1L2	chr16:79731290	chr16:79731920	DEL	608	99	6
Patient 3	BANP	BANP	chr16:86644868	chr16:86645285	DEL	689	99	13
Patient 3	intergenic	intergenic	chr16:86868821	chr16:86870047	DEL	1224	99	6
Patient 3	intergenic	intergenic	chr17:20593	chr17:21743	DEL	1070	99	9
Patient 3	GARNL4	GARNL4	chr17:2850496	chr17:2851608	DEL	917	99	6
Patient 3	NT5M	NT5M	chr17:17171095	chr17:17171950	DEL	953	99	12
Patient 3	FOXN1	FOXN1	chr17:23867813	chr17:23868292	DEL	469	99	9
Patient 3	intergenic	intergenic	chr17:36675288	chr17:36685740	DEL	10396	99	10
Patient 3	MAP2K4	SAMD14	chr17:11978131	chr17:45545035	DEL	33566908	99	6
Patient 3	FAM117A	FAM117A	chr17:45181809	chr17:45182819	DEL	1159	89	5
Patient 3	intergenic	intergenic	chr17:50818297	chr17:50820295	DEL	2162	99	5
Patient 3	intergenic	ROCK1	chr18:96882	chr18:101679	ITX	1036	99	9
Patient 3	intergenic	intergenic	chr17:78606061	chr17:78606766	DEL	570	99	5
Patient 3	intergenic	intergenic	chr17:78653116	chr17:78654350	DEL	1141	99	7
Patient 3	intergenic	intergenic	chr1:121186859	chr18:16773251	CTX	-488	80	15
Patient 3	intergenic	intergenic	chr18:50577019	chr18:50577673	DEL	654	99	7
Patient 3	ZNF407	ZNF407	chr18:70756604	chr18:70757279	DEL	614	99	7
Patient 3	intergenic	intergenic	chr18:74474615	chr18:74475585	DEL	949	99	9
Patient 3	intergenic	intergenic	chr18:74696037	chr18:74696774	DEL	568	99	6
Patient 3	intergenic	intergenic	chr19:345206	chr19:345985	DEL	872	99	9
Patient 3	intergenic	intergenic	chr19:2664103	chr19:2665393	DEL	1092	99	10
Patient 3	intergenic	intergenic	chr19:2664601	chr19:2665393	DEL	684	99	5
Patient 3	PIAS4	PIAS4	chr19:3987104	chr19:3987797	DEL	472	99	6
Patient 3	KIAA1881	KIAA1881	chr19:4462007	chr19:4462312	DEL	497	99	7
Patient 3	intergenic	intergenic	chr1:121186859	chr19:32424972	CTX	-488	99	98
Patient 3	intergenic	intergenic	chr1:121186859	chr19:32430240	CTX	-488	99	130
Patient 3	intergenic	intergenic	chr6:58887220	chr19:32423663	CTX	-488	99	36
Patient 3	intergenic	intergenic	chr7:1607276	chr19:32423663	CTX	-488	99	41
Patient 3	intergenic	intergenic	chr19:23847289	chr19:23941836	DEL	95129	97	5
Patient 3	intergenic	intergenic	chr19:35979329	chr19:35981656	DEL	2378	99	10
Patient 3	intergenic	intergenic	chr19:61283165	chr19:61283821	DEL	472	99	10
Patient 3	PSMF1	PSMF1	chr20:1043189	chr20:1043961	DEL	571	99	5
Patient 3	intergenic	intergenic	chr20:1943402	chr20:1945611	DEL	2110	99	9
Patient 3	intergenic	intergenic	chr20:18138095	chr20:18139242	DEL	977	99	5
Patient 3	intergenic	intergenic	chr20:18138670	chr20:18139242	DEL	666	99	6
Patient 3	intergenic	LOC283788	chr4:190437934	chr20:28266143	CTX	-488	99	22
Patient 3	intergenic	intergenic	chr20:46277084	chr20:46648173	INV	370702	99	5
Patient 3	CDH4	CDH4	chr20:59337732	chr20:59337825	ITX	-420	99	24
Patient 3	intergenic	intergenic	chr20:59979528	chr20:59980102	DEL	578	99	8
Patient 3	intergenic	intergenic	chr20:61737466	chr20:61740154	DEL	635	97	6
Patient 3	intergenic	intergenic	chr21:9846957	chr21:9849986	DEL	3057	99	8
Patient 3	KCNJ6	KCNJ6	chr21:38051077	chr21:38051635	DEL	611	99	14
Patient 3	TRPM2	TRPM2	chr21:44654392	chr21:44655302	DEL	763	99	7

Patient 3	intergenic	intergenic	chr21:45272557	chr21:45273070	DEL	693	95	5
Patient 3	PCBP3	PCBP3	chr21:46168645	chr21:46169536	DEL	716	99	5
Patient 3	CECR5	CECR5	chr22:16007255	chr22:16008220	DEL	891	99	10
Patient 3	intergenic	intergenic	chr22:45380501	chr22:45381096	DEL	508	99	5
Patient 3	MAGT1	MAGT1	chrX:77008083	chrX:77010572	DEL	2488	99	7
Patient 3	intergenic	intergenic	chrY:57385646	chrY:57390339	ITX	3144	99	7
Patient 3	intergenic	intergenic	chrY:57395311	chrY:57403554	ITX	3843	99	13
Patient	Gene1	Gene2	Genomic position 1	Genomic position 2	Type	Size	Score	Supporting Reads
Patient 4	intergenic	AK055150	chr1:47776650	chr1:59034813	INV	11257307	99	13
Patient 4	intergenic	DAB1	chr1:51204946	chr1:58694514	INV	7489047	99	5
Patient 4	intergenic	intergenic	chr1:51218059	chr1:59372492	INV	8153933	99	8
Patient 4	intergenic	intergenic	chr1:109988639	chr1:109992894	DEL	4285	99	8
Patient 4	CR936796,BC053679,BC029473,LOC375010	CR936796,B053679,BC029473,LOC375010	chr1:141826811	chr1:141827809	ITX	-404	93	5
Patient 4	NBPF20,PDE4DIP,KIAA1245,NBPF8,NBPF14,NBPF10	NBPF20,PD E4DIP,KIAA1245,NBPF8,NBPF14,NBPF10	chr1:143605459	chr1:143606454	DEL	1023	99	7
Patient 4	NBPF20,PDE4DIP,KIAA1245,NBPF8,NBPF14,NBPF10	NBPF20,PD E4DIP,KIAA1245,NBPF8,NBPF14,NBPF10	chr1:143607628	chr1:143618164	DEL	10437	99	8
Patient 4	intergenic	intergenic	chr1:167270977	chr1:167271915	DEL	937	99	9
Patient 4	IDN4-GGTR7,KIAA0471,RABGAP1L	IDN4-GGTR7,KIAA0471,RABGAP1L	chr1:173063130	chr1:173068484	DEL	5341	99	6
Patient 4	AK125248	intergenic	chr1:714790	chr1:222268927	ITX	-64778127	99	15
Patient 4	intergenic	intergenic	chr2:2777696	chr2:2778282	DEL	499	99	5
Patient 4	ALLC	ALLC	chr2:3697014	chr2:3698172	DEL	873	99	5
Patient 4	intergenic	intergenic	chr2:10070511	chr2:10072848	ITX	1272	99	6
Patient 4	intergenic	intergenic	chr2:39713449	chr2:39716796	DEL	3242	99	5
Patient 4	intergenic	intergenic	chr2:51780050	chr2:51781290	DEL	1211	99	8
Patient 4	BC041356	intergenic	chr2:64692902	chr2:65014903	ITX	320889	91	5
Patient 4	intergenic	intergenic	chr2:90960217	chr2:90966505	DEL	6481	99	6
Patient 4	intergenic	intergenic	chr2:90963056	chr2:90975734	ITX	3607	99	6
Patient 4	intergenic	intergenic	chr2:161843240	chr2:161847276	ITX	3161	99	5
Patient 4	intergenic	intergenic	chr2:173262690	chr2:173264483	DEL	1789	99	10
Patient 4	intergenic	intergenic	chr2:195005341	chr2:195006706	DEL	1351	99	6
Patient 4	intergenic	intergenic	chr2:238869443	chr2:238870027	DEL	553	99	7
Patient 4	intergenic	intergenic	chr3:34924538	chr3:35246285	DEL	321709	99	5
Patient 4	intergenic	intergenic	chr3:68822319	chr3:68830628	DEL	8227	99	6
Patient 4	intergenic	intergenic	chr3:75359989	chr3:75361624	DEL	2074	99	8
Patient 4	ABI3BP	ABI3BP	chr3:102004247	chr3:102005267	DEL	922	99	6
Patient 4	intergenic	intergenic	chr3:112726227	chr3:112731799	DEL	5376	99	5
Patient 4	intergenic	intergenic	chr3:120833277	chr3:120836810	DEL	3565	99	7
Patient 4	intergenic	intergenic	chr3:120902567	chr3:120903057	DEL	468	99	8
Patient 4	intergenic	intergenic	chr3:147867860	chr3:147873108	DEL	4965	99	7
Patient 4	KCNAB1	KCNAB1	chr3:157575065	chr3:157576321	DEL	1583	99	7
Patient 4	intergenic	intergenic	chr3:193271964	chr3:193272768	DEL	646	99	9
Patient 4	intergenic	ATP8A1	chr4:42077721	chr4:42208594	INV	130378	99	6
Patient 4	intergenic	intergenic	chr1:142120283	chr4:49207021	CTX	-530	99	62
Patient 4	intergenic	intergenic	chr4:48805538	chr4:48815749	DEL	10134	99	12
Patient 4	intergenic	intergenic	chr4:60007317	chr4:60013851	ITX	5390	99	5
Patient 4	intergenic	intergenic	chr4:60498908	chr4:60500606	DEL	1615	99	5
Patient 4	intergenic	intergenic	chr4:61621570	chr4:61624836	DEL	3110	99	5
Patient 4	intergenic	intergenic	chr4:115727166	chr4:115733425	DEL	6028	99	6
Patient 4	TTC29	TTC29	chr4:147949585	chr4:147950576	DEL	962	99	6

Patient 4	intergenic	intergenic	chr4:179163374	chr4:179164291	ITX	-474	99	17
Patient 4	intergenic	intergenic	chr4:184892815	chr4:184896105	DEL	3192	99	5
Patient 4	intergenic	intergenic	chr4:190823056	chr4:190850738	INV	26824	99	42
Patient 4	CLPTM1L	CLPTM1L	chr5:1386389	chr5:1386684	ITX	-440	99	6
Patient 4	intergenic	intergenic	chr5:7969766	chr5:7973591	DEL	3566	99	6
Patient 4	intergenic	intergenic	chr5:10326274	chr5:10328377	DEL	1908	99	9
Patient 4	CTNND2	CTNND2	chr5:11869755	chr5:11870578	DEL	586	99	5
Patient 4	11-Mar	11-Mar	chr5:16177793	chr5:16178492	DEL	652	99	6
Patient 4	intergenic	intergenic	chr5:30951207	chr5:30951644	DEL	581	99	8
Patient 4	intergenic	intergenic	chr5:50270118	chr5:50275008	DEL	5146	99	9
Patient 4	intergenic	intergenic	chr5:61610470	chr5:61612329	DEL	1707	99	6
Patient 4	intergenic	intergenic	chr5:86281720	chr5:86282898	DEL	1131	99	7
Patient 4	intergenic	intergenic	chr6:116717	chr6:118649	DEL	1968	99	9
Patient 4	HLA-A*0226,AK097 625	HLA-A*0226,AK0 97625	chr6:30007752	chr6:30009556	DEL	1824	99	7
Patient 4	intergenic	intergenic	chr6:31319580	chr6:31321125	DEL	1554	99	5
Patient 4	intergenic	intergenic	chr6:32485813	chr6:32486692	DEL	871	99	6
Patient 4	PKHD1	PKHD1	chr6:51847392	chr6:51853574	DEL	6053	99	7
Patient 4	intergenic	intergenic	chr6:69198864	chr6:69199833	DEL	992	99	8
Patient 4	intergenic	intergenic	chr6:74648755	chr6:74659304	DEL	10433	99	5
Patient 4	WASF1	WASF1	chr6:110583413	chr6:110586475	DEL	3089	99	7
Patient 4	C6orf204	C6orf204	chr6:119118427	chr6:119120861	ITX	1101	99	9
Patient 4	intergenic	intergenic	chr6:159888165	chr6:159890835	DEL	2687	99	6
Patient 4	intergenic	intergenic	chr6:160006516	chr6:160008697	DEL	2493	99	6
Patient 4	intergenic	intergenic	chr6:167795034	chr6:167795262	ITX	-473	99	6
Patient 4	DACT2	DACT2	chr6:168459835	chr6:168461586	DEL	1602	99	10
Patient 4	intergenic	intergenic	chr6:169951927	chr6:169952281	DEL	417	99	9
Patient 4	SDK1	SDK1	chr7:3620944	chr7:3622108	DEL	1156	99	5
Patient 4	SDK1	SDK1	chr7:3969078	chr7:3969907	DEL	574	99	5
Patient 4	intergenic	intergenic	chr7:15851930	chr7:15852416	DEL	499	99	5
Patient 4	intergenic	intergenic	chr7:61272031	chr7:61275180	ITX	2092	99	7
Patient 4	intergenic	intergenic	chr7:61463848	chr7:61464688	DEL	566	99	5
Patient 4	LHFPL3	LHFPL3	chr7:104039694	chr7:104041145	DEL	1445	99	6
Patient 4	intergenic	intergenic	chr7:144547982	chr7:144552361	DEL	4568	99	7
Patient 4	PTPRN2	PTPRN2	chr7:157739150	chr7:157740114	DEL	797	99	6
Patient 4	intergenic	intergenic	chr7:158193406	chr7:158197556	DEL	4065	99	8
Patient 4	intergenic	intergenic	chr7:158691640	chr7:158692277	DEL	726	99	12
Patient 4	intergenic	intergenic	chr8:1282113	chr8:1282471	ITX	-447	99	7
Patient 4	intergenic	intergenic	chr8:16866249	chr8:16866731	DEL	410	99	13
Patient 4	intergenic	intergenic	chr8:78803827	chr8:78806159	DEL	2209	99	5
Patient 4	intergenic	intergenic	chr8:96944284	chr8:96948760	DEL	4398	99	5
Patient 4	ANGPT1	ANGPT1	chr8:108573996	chr8:108575536	DEL	1567	99	5
Patient 4	intergenic	intergenic	chr8:132311939	chr8:132312576	DEL	596	99	5
Patient 4	intergenic	intergenic	chr9:13561295	chr9:13565998	DEL	4683	99	9
Patient 4	intergenic	intergenic	chr9:86964930	chr9:86965721	DEL	990	99	5
Patient 4	intergenic	intergenic	chr9:90598399	chr9:90599154	DEL	851	99	6
Patient 4	intergenic	intergenic	chr9:91365809	chr9:91367823	DEL	1976	99	6
Patient 4	intergenic	intergenic	chr9:110049757	chr9:110050007	ITX	-453	99	7
Patient 4	intergenic	intergenic	chr9:128560551	chr9:128563091	DEL	2816	99	9
Patient 4	intergenic	intergenic	chr10:829665	chr10:830197	DEL	408	99	7
Patient 4	intergenic	intergenic	chr11:121186859	chr10:41720214	CTX	-530	99	14
Patient 4	intergenic	intergenic	chr11:121186859	chr10:41848996	CTX	-530	99	15
Patient 4	intergenic	intergenic	chr10:41705727	chr10:41712243	DEL	7044	99	11
Patient 4	intergenic	intergenic	chr10:41706959	chr10:41716990	ITX	8210	93	6
Patient 4	PBLD	PBLD	chr10:69738151	chr10:69740699	DEL	2475	99	6
Patient 4	TCERG1L	TCERG1L	chr10:132977751	chr10:132978425	DEL	403	99	7
Patient 4	KIAA1674,LR RC27	KIAA1674,L RRC27	chr10:134015305	chr10:134016204	DEL	691	99	5
Patient 4	intergenic	intergenic	chr11:184592	chr11:184752	ITX	-479	99	5
Patient 4	SBF2,KIAA176 6	SBF2,KIAA1 766	chr11:10249291	chr11:10250432	DEL	1165	99	9
Patient 4	intergenic	intergenic	chr11:20525709	chr11:20527884	DEL	2045	99	7
Patient 4	intergenic	intergenic	chr11:35226797	chr11:35226847	ITX	-449	99	6

Patient 4	intergenic	intergenic	chr11:48557440	chr11:48560882	DEL	3469	99	11
Patient 4	intergenic	intergenic	chr11:48899133	chr11:48900242	DEL	1264	96	5
Patient 4	intergenic	intergenic	chr11:50318443	chr11:50321873	ITX	2328	99	7
Patient 4	intergenic	intergenic	chr11:54750471	chr11:54750931	DEL	401	99	5
Patient 4	intergenic	intergenic	chr11:63455918	chr11:63458051	DEL	2699	99	6
Patient 4	intergenic	intergenic	chr11:65775167	chr11:65777351	INV	471	99	8
Patient 4	intergenic	intergenic	chr11:128187922	chr11:128188691	DEL	738	99	8
Patient 4	intergenic	intergenic	chr11:134079628	chr11:134079873	ITX	-486	99	5
Patient 4	intergenic	intergenic	chr11:1341110371	chr11:134111101	DEL	692	99	6
Patient 4	WNK1	WNK1	chr12:737025	chr12:745044	DEL	8041	99	5
Patient 4	intergenic	intergenic	chr12:24832141	chr12:24832955	DEL	739	99	9
Patient 4	intergenic	intergenic	chr12:34093888	chr12:37025977	DEL	2931815	99	6
Patient 4	intergenic	intergenic	chr12:58222030	chr12:58232908	DEL	10741	99	5
Patient 4	intergenic	intergenic	chr12:89749706	chr12:89751343	ITX	595	99	7
Patient 4	intergenic	intergenic	chr13:25948030	chr13:25950322	DEL	2141	99	5
Patient 4	intergenic	intergenic	chr13:26817286	chr13:26817691	DEL	416	99	6
Patient 4	PCDH9	PCDH9	chr13:66072731	chr13:66075449	DEL	2712	99	5
Patient 4	intergenic	intergenic	chr13:70715332	chr13:70718323	DEL	2956	99	9
Patient 4	intergenic	intergenic	chr13:82686209	chr13:82690630	DEL	4381	99	7
Patient 4	IRS2	IRS2	chr13:109215805	chr13:109217136	DEL	1075	99	5
Patient 4	FAM70B	FAM70B	chr13:113620166	chr13:113620832	DEL	417	99	6
Patient 4	intergenic	intergenic	chr14:53780044	chr14:53783426	DEL	3390	99	10
Patient 4	intergenic	intergenic	chr15:68381923	chr15:68382617	ITX	-503	99	11
Patient 4	intergenic	intergenic	chr15:77591759	chr15:77592335	DEL	419	99	7
Patient 4	intergenic	intergenic	chr16:13201966	chr16:13203988	DEL	2055	99	11
Patient 4	NT5M	NT5M	chr17:17171109	chr17:17171998	DEL	918	99	10
Patient 4	intergenic	intergenic	chr17:36675277	chr17:36685732	DEL	10380	99	6
Patient 4	intergenic	intergenic	chr17:38792075	chr17:38797925	ITX	4915	99	7
Patient 4	FSHR	WIP1	chr2:49219584	chr17:63944101	CTX	-530	99	12
Patient 4	intergenic	intergenic	chr18:74474629	chr18:74475442	DEL	909	99	12
Patient 4	DKFZp434A042,ATP9B	DKFZp434A042,ATP9B	chr18:75188486	chr18:75188868	ITX	-448	99	5
Patient 4	ZNF826	intergenic	chr19:20387593	chr19:20509515	DEL	122164	99	8
Patient 4	intergenic	intergenic	chr19:20547715	chr19:20744110	INV	195894	99	5
Patient 4	intergenic	intergenic	chr1:121186859	chr19:32424972	CTX	-530	99	73
Patient 4	intergenic	intergenic	chr1:121186859	chr19:32425650	CTX	-530	99	23
Patient 4	intergenic	intergenic	chr1:121186859	chr19:32430242	CTX	-530	99	222
Patient 4	intergenic	intergenic	chr20:6922273	chr20:6924929	DEL	2649	99	5
Patient 4	intergenic	LOC283788	chr4:190438032	chr20:28267052	CTX	-530	99	18
Patient 4	intergenic	intergenic	chr20:36715109	chr20:36715225	ITX	-462	99	5
Patient 4	intergenic	intergenic	chr20:46277156	chr20:46648175	INV	370534	99	6
Patient 4	TSHZ2	TSHZ2	chr20:51254027	chr20:51254103	ITX	-462	99	6
Patient 4	CDH4	CDH4	chr20:59337731	chr20:59337827	ITX	-457	99	20
Patient 4	LOC554226	intergenic	chr2:132722168	chr21:9729240	ITX	-464	99	6
Patient 4	RTEL1	RTEL1	chr20:61771456	chr20:61772176	DEL	457	99	6
Patient 4	intergenic	intergenic	chr21:9869501	chr21:9869931	DEL	666	99	9
Patient 4	intergenic	intergenic	chr21:39397360	chr21:39401538	DEL	4162	99	6
Patient 4	C2CD2	C2CD2	chr21:42223193	chr21:42226609	DEL	3394	99	11
Patient 4	TUBA8	TUBA8	chr22:16998962	chr22:17005911	ITX	5530	90	5
Patient 4	THEM2	SYN3	chr6:24792550	chr22:31257881	CTX	-530	99	17
Patient 4	intergenic	intergenic	chr22:37374276	chr22:37374707	DEL	424	99	5
Patient 4	FAM19A5	FAM19A5	chr22:47450010	chr22:47450972	DEL	847	99	7
Patient 4	intergenic	intergenic	chrX:81868941	chrX:81874966	DEL	5796	99	13
Patient 4	intergenic	intergenic	chrX:93846199	chrX:97665992	ITX	3818962	99	5
Patient 4	intergenic	intergenic	chrX:147317118	chrX:147318950	DEL	1587	99	6
Patient 4	intergenic	intergenic	chrX:152308264	chrX:152309904	ITX	438	99	6
Patient 4	ROCK1	intergenic	chr18:101447	chrY:11920815	CTX	-530	99	63
Patient 4	intergenic	intergenic	chrY:57394498	chrY:57401020	ITX	3857	99	14
Patient 4	intergenic	intergenic	chrY:11757912	chrY:11758504	DEL	782	99	5

**Table S14: Patient 1 Gene Fusions nominated by RNA-Seq**

5' transcript	3' transcript	Fusion Genes	Type	Distance	Total Supporting Reads	Breakpoint Spanning Reads
uc003eom.2	uc003enx.2	CPNE4 NEK11	Intrachromosomal_Complex	-359604	754	186
uc003ehn.3	uc003eey.2	TMPRSS2 ERG	Intrachromosomal_Complex	-2347138	120	115
uc003jrh.3	uc001xdz.1	GPBP1 DAAM1	Interchromosomal	NA	78	27
uc002yzj.2	uc002yxa.2	UMPS CCDC58	Intrachromosomal	-2966050	57	25
uc002ozv.2	uc002pnc.2	PVRL2 CD37	Intrachromosomal	4456230	43	3
uc003vrk.2	uc002hqd.2	EXOC4 SNIP	Interchromosomal	NA	30	21
uc002ilr.3	uc002jdz.2	NPEPPS ERN1	Intrachromosomal_Complex	16419748	13	9
uc001xiw.2	uc010vwd.1	GPHN PIGL	Interchromosomal	NA	9	4

**Table S15: Patient 2 Gene Fusions nominated by RNA-Seq**

5' transcript	3' transcript	Fusion Genes	Type	Distance	Total Supporting Reads	Breakpoint Spanning Reads
uc002gij.2	uc001wqm.1	TP53 SCFD1	Interchromosomal	NA	1622	530
uc010gor.2	uc002yxc.3	TMPRSS2 ERG	Intrachromosomal	-2802774	1466	414
uc001vqx.2	uc003tfu.3	COL4A2 TARP	Interchromosomal	NA	496	324
uc002vnj.2	uc002gmp.3	ACSL3 MYH2	Interchromosomal	NA	285	169
uc001wqm.1	uc010cnk.1	SCFD1 TP53	Interchromosomal	NA	130	82
uc003frq.1	uc003csj.1	BCL6 CAMP	Intrachromosomal_Complex	-139172189	52	0
uc002zdv.2	uc002yzj.2	AGPAT3 TMPRSS2	Intrachromosomal_Complex	-2405030	48	5
uc002gkg.3	uc002vni.2	TMEM107 ACSL3	Interchromosomal	NA	34	13
uc003qmj.2	uc003qmq.1	MAP3K7IP2 C6orf72	Read_Through	154779	27	22
uc009zrj.2	uc001sxq.1	FRS2 GLIPR1L2	Intrachromosomal	5811327	24	4
uc002vtg.2	uc002vvs.2	GIGYF2 AGAP1	Intrachromosomal	2718040	22	7
uc002lpp.2	uc001ztj.1	PTBP1 FRMD5	Interchromosomal	NA	16	3
uc001yva.2	uc002mee.1	NIPA2 ACSBG2	Interchromosomal	NA	10	1

**Table S16: Patient 3 Gene Fusions nominated by RNA-Seq**

5' transcript	3' transcript	Fusion Genes	Type	Distance	Total Supporting Reads	Breakpoint Spanning Reads
uc004cpv.2	uc004cpf.2	PP1164 PPP2R3B	Intrachromosomal_Complex	-1216833	145	97
uc003xmr.2	uc003xjw.2	ADAM9 KCNU1	Intrachromosomal	-2063954	11	0

**Table S17: Patient 4 Gene Fusions nominated by RNA-Seq**

5' transcript	3' transcript	Fusion Genes	Type	Distance	Total Supporting Reads	Breakpoint Spanning Reads
uc002jhd.3	uc002rww.2	WIPI1 FSHR*	Interchromosomal	NA	386	232
uc002rww.2	uc001csg.2	FSHR CDKN2C*	Interchromosomal	NA	55	10
uc003xpe.2	uc002hku.2	SLC20A2 CCL18	Interchromosomal	NA	16	5
uc002jxs.2	uc002rut.2	EIF4A3 PRKCE	Interchromosomal	NA	8	8

\*Complex rearrangement involving WIPI1, FSHR, and CDKN2C